

191509

From: Hamud, Fozia
Sent: Wednesday, May 31, 2006 1:28 PM
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Subject: sequence search 10/732,796

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Kindly search SEQ ID NOs: 11 and 12 of 10/732,796 against commercial and interference data bases. thank you.

FOZIA HAMUD
PATENT EXAMINER
ART UNIT 1647
ROOM:REM 4D64
MAIL BOX: REM 4C70

WFOZIA

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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QY 361 TQNVFDSIEPKCSTIWKLETLILOKNGLKDFKGMLMTKOMPSLBDYWSNSLESGRH 420
 Db 367 TQNVFDSIEPKCSTIWKLETLILOKNGLKDFKGMLMTKOMPSLBDYWSNSLESGRH 426
 QY 421 KENCTWVESTIVLNLSNMLTDSVFRCLPPLPKVLDHSNKIKSVPKVQVKLEALQELNV 480
 Db 427 KENCTWVESTIVLNLSNMLTDSVFRCLPPLPKVLDHSNKIKSVPKVQVKLEALQELNV 486
 QY 481 AFNSLTDLPGCGSFSSLVILDHNSVSHPAFFOSCORSKRISAGDNPFQTCBREF 540
 Db 487 AFNSLTDLPGCGSFSSLVILDHNSVSHPAFFOSCORSKRISAGDNPFQTCBREF 546
 QY 541 VKNIDOVSESVLEGWDSDSYKDYPESYRGSPKDFMSELSCNTILIVIGATMLVAV 600
 Db 547 VKNIDOVSESVLEGWDSDSYKDYPESYRGSPKDFMSELSCNTILIVIGATMLVAV 606
 QY 601 TVTSCLCYLDLFWYLWLMCOMTOTRRARNIPPLEORNLQPHAFISYSEHDSAWKSEL 660
 Db 607 TVTSCLCYLDLFWYLWLMCOMTOTRRARNIPPLEORNLQPHAFISYSEHDSAWKSEL 666
 QY 661 VPYLEKEDEIQICLHERNFVPGKSIVENINIEKSYKISIPFSPNFSVQEWCHYLYFAH 720
 Db 667 VPYLEKEDEIQICLHERNFVPGKSIVENINIEKSYKISIPFSPNFSVQEWCHYLYFAH 726
 QY 721 HNLFHGSNNLILLEPIQNSIPNKHKUKALMORTYIOWPKEKSKRGLFWANIRAA 780
 Db 727 HNLFHGSNNLILLEPIQNSIPNKHKUKALMORTYIOWPKEKSKRGLFWANIRAA 786
 QY 781 FMKLUVTENDVKS 796
 Db 787 FMKLUVTENDVKS 802

RESULT 2
 US-09-949-002-386
 ; Sequence 386 Application US/09949002
 ; Patent No. 6900016
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CL000790
 ; CURRENT APPLICATION NUMBER: US/09/949, 002
 ; CURRENT FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/231, 401
 ; NUMBER OF SEQ ID NOS: 10823
 ; SEQ ID NO: 386
 ; LENGTH: 796
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-002-386

Query Match 99.9%; Score 4149; DB 2; Length 796;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTKDKEPIVKSPHFVCMIIITGTRIQFSDSNEFAFDKSKRGLIHVPDKLPLTKYLDMS 60
 Db 1 MTKDKEPIVKSPHFVCMIIITGTRIQFSDSNEFAFDKSKRGLIHVPDKLPLTKYLDMS 60
 QY 61 ONYIARLQVSMSFSLBLTURLHSRIOQLDLSVFKNOOLEYLDLISHNOLQKISCHPI 120
 Db 61 ONYIARLQVSMSFSLBLTURLHSRIOQLDLSVFKNOOLEYLDLISHNOLQKISCHPI 120
 QY 121 WSFRHDLDFNDPKAIPICKERGNLSQNLNFGLSAMKLOQDLPFLAHHSYIILDLRN 180
 Db 121 WSFRHDLDFNDPKAIPICKERGNLSQNLNFGLSAMKLOQDLPFLAHHSYIILDLRN 180
 QY 181 YYIKENETESTSQILNAKTHLFVHTSLFQIWNISNTGCLQTNKUNDNCQVFIK 240

Db 181 YYIKENETESTSQILNAKTHLFVHTSLFQIWNISNTGCLQTNKUNDNCQVFIK 240
 QY 241 FLSELTRGSTLNFNLHBTWKCLVRVQFLWKPVEVNTYMLTIESIREDFTY 300
 Db 241 FLSELTRGPTLNFNLHBTWKCLVRVQFLWKPVEVNTYMLTIESIREDFTY 300
 QY 301 KTKALKLTIEHTINQFLSOTALYTFSENNIMMLTISPTF1HMLCPHAPSTFELNF 360
 Db 301 KTKALKLTIEHTINQFLSOTALYTFSENNIMMLTISDTPTF1HMLCPHAPSTFELNF 360
 QY 361 TQNVFDSIEPKCSTIWKLETLILOKNGLKDFKGMLMTKOMPSLBDYWSNSLESGRH 420
 Db 361 TQNVFDSIEPKCSTIWKLETLILOKNGLKDFKGMLMTKOMPSLBDYWSNSLESGRH 420
 QY 421 KENCTWVESTIVLNLSNMLTDSVFRCLPPLPKVLDHSNKIKSVPKVQVKLEALQELNV 480
 Db 421 KENCTWVESTIVLNLSNMLTDSVFRCLPPLPKVLDHSNKIKSVPKVQVKLEALQELNV 480
 QY 481 AFNSLTDLPGCGSFSSLVILDHNSVSHPAFFOSCORSKRISAGDNPFQTCBREF 540
 Db 481 AFNSLTDLPGCGSFSSLVILDHNSVSHPAFFOSCORSKRISAGDNPFQTCBREF 540
 QY 541 VKNIDOVSESVLEGWDSDSYKDYPESYRGSPKDFMSELSCNTILIVIGATMLVAV 600
 Db 541 VKNIDOVSESVLEGWDSDSYKDYPESYRGSPKDFMSELSCNTILIVIGATMLVAV 600
 QY 601 TVTSCLCYLDLFWYLWLMCOMTOTRRARNIPPLEORNLQPHAFISYSEHDSAWKSEL 660
 Db 601 TVTSCLCYLDLFWYLWLMCOMTOTRRARNIPPLEORNLQPHAFISYSEHDSAWKSEL 660
 QY 661 VPYLEKEDEIQICLHERNFVPGKSIVENINIEKSYKISIPFSPNFSVQEWCHYLYFAH 720
 Db 661 VPYLEKEDEIQICLHERNFVPGKSIVENINIEKSYKISIPFSPNFSVQEWCHYLYFAH 720
 QY 721 HNLFHGSNNLILLEPIQNSIPNKHKUKALMORTYIOWPKEKSKRGLFWANIRAA 780
 Db 721 HNLFHGSNNLILLEPIQNSIPNKHKUKALMORTYIOWPKEKSKRGLFWANIRAA 780
 QY 781 FMKLUVTENDVKS 796
 Db 781 FMKLUVTENDVKS 796

RESULT 3
 US-09-949-002-351
 ; Sequence 351 Application US/09949002
 ; Patent No. 6900016
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CL000790
 ; CURRENT APPLICATION NUMBER: US/09/949, 002
 ; CURRENT FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/231, 401
 ; NUMBER OF SEQ ID NOS: 10823
 ; SEQ ID NO: 351
 ; LENGTH: 786
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-002-351

Query Match 68.1%; Score 2830; DB 2; Length 786;
 Best Local Similarity 69.5%; Pred. No. 1e-262; Mismatches 540; Conservative 92; Mismatches 143; Indels 2; Gaps 1;

QY 12 FHFVCMIIITGTRIQFSDSNEFAFDKSKRGLIHVPDKLPLTKYLDMSONYIAELOQSD 71
 Db 5 FHFVCMIIITGTRIQFSDSNEFAFDKSKRGLIHVPDKLPLTKYLDMSONYIAELOQSD 64

Best Local Similarity 70.3%; Pred. No. 3.7e-227; Matches 469; Conservative 73; Mismatches 123; Indels 2; Gaps 1;

Qy	72 NSPLSELIVLVRISHNRIOQLDLSVFKENQDIEYLDISHNQOQKISCHPIVSFRHLDIFN 131
Db	65 TISLSKURILITISHNRIOQLDLSVFKENQDIEYLDISHNQKVKISCHPTWVLKHLDFN 124
Qy	132 AFDALPICKERGFLNSQNLFLGLSAMKLUQKLDPITAHLSYLDRNNTYIKENTESL 191
Db	125 AFDALPICKERGFLNSQNLFLGLSAMKLUQKLDPITAHLSYLDRNNTYIKENTESL 184
Qy	192 QLNAKTHLUVHPTSLFAIQVNISNTLGCOLQINTK-LANDNCVFIPLSTLRGS 249
Db	185 QDNFTESLHVVEPTNKKEFHFLDVSKVVAUNELSNKCVLEDNKSYFSLIQLQNP 244
Qy	250 TLFNFTLHETTWKCLVRFQFLWPKVEVANINYNTIESIREDFTYKTTLKALI 309
Db	245 KLSLSLTANNIETTWNFSRILOLWHITWVWVSISSNVKLGQOLDFRDFDYGTSIHLASI 304
Qy	310 HATINOVFLFQTALEYVFSNIMMUTISDFPFLMCPAPSTEXFLNTIONVTDSI 369
Db	305 HOVSDVFGFPOSYIVBFSNNNIKNFVSGTRMVMHLCPSKSPFLHLDISNNLLDTV 364
Qy	370 PEKCASTVUKELLIQNGKLDFKVLGMTKOMPSCBLSIDWSNSLESGRKENCWES 429
Db	365 FENGCHLTTELITLLOMNLQKLSKAEMTOMQSKISQDLSQNSYDEKRGDCWTKS 424
Qy	430 IVVNLTSNNMUDSVRCLPRTKVUDLHSNKKSVRKQVVKLAEQBLNTAFNSLTDLP 489
Db	425 LLSLNHNSSNLITUTIFCRCLPRTKVUDLHSNKKSFQVVKLAEQBLNTAFNSLTDLP 484
Qy	490 GCGSFPSLISVLLDHNSVSHSADEFOSCQNSRISTKAGDNPFQCTBLREVKNIQVS 549
Db	485 GCGSFSSLISVLLTDHSVSHSADEFOSCQNSRISTKAGDNPFQCTBLREVKNIQVS 544
Qy	550 ELEGMPDSYKDYPESYRGSLDKFMSLSCNITLIVITGATMVLATMVLATVSCYL 609
Db	545 ELEGMPDSYKDYPESYRGSLDKFMSLSCNITLIVITGATMVLATMVLATVSCYL 604
Qy	610 DLFWYLRMVCQMTOTERRARNPBLEQLQRNTQPHAFISYSSEHDASAWYKSELVPLEKDI 669
Db	605 DLFWYLRMVCQMTOTERRARNPBLEQLQRNLOFAHFSYSGHDSFWKVNELLPNLKEGM 664
Qy	670 QICLHERNFWVCKSIVENITTCIEKSYKSIIVLSPNQVOSWCHYELYFAHNLFIRGSN 729
Db	665 QICLHERNFWVCKSIVENITTCIEKSYKSIIVLSPNQVOSWCHYELYFAHNLFIRGSN 724
Qy	730 NLLLLEPIONSIPKYHKULAMTQYLQWPKEKSKRGLFWANIRAAFNKLT 786
Db	725 SLLLLEPIQYISSLSSYHKLSMARRTIVLWPEKSKRGLFWANIRAAFNKLT 781
Qy	780 AFNMKLT 786
Db	661 AINIKLT 667

RESULT 4
US-09-949-002-522

; Sequence 522, Application US/09949002

; Patent No. 600015

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL000790

; CURRENT APPLICATION NUMBER: US/09/949, 002

; CURRENT FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/231, 401

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 10823

; SOFTWARE: FastSEQ for Windows version 4.0

; SEQ ID NO: 522

; LENGTH: 672

; TYPE: PRT

; ORGANISM: Human

; US-09-949-002-522

Query Match 59.2%; Score 2459; DB 2; Length 672;

RESULT 5
US-09-991-181-57

; Sequence 57, Application US/09991181

; Patent No. 6913919

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Guiney, Austin L.

; APPLICANT: KJavvin, Ivar J.

; APPLICANT: Napior, Maty A.

; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P27301C53
 CURRENT APPLICATION NUMBER: US/09/991.181
 CURRENT FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
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 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090540
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557

QY 247 RGSTILN----FTLHIELTWKCLVRYQFOFLWPKPVPEVINYNTI--JESIREDFTY 299
 QY 235 RNUISLENAKTSVUJLNUKVUDLWDLFLIQFWHMSVHSERHQIRWTFGKAYLDINSFDY 294
 Db 300 SKTTKALTIETHTNQVFLPSOTAMLYTVESEMMINTMLTSDFTPFIMLCPHAPSTPKFLN 359
 QY 295 SNTVMTIKLEHFFRUVFTIQQDXYLITKNDENLTISNAQMPHMLFENPFTKQYLN 354
 QY 360 FTCONVFTSIFEKCSTLVKLETIILQKNGKLDFLGVLMTKDMPSLLELDVMSWNSLSGR 419
 QY 355 FANNITLTDLFKRITOLPHKTLTINGKLETLSLVSCFAINTP-LIEHLDSLONLIQH-K 412
 Db 420 HKENCTTWWESIVVNLNSSLSSMLTDSVFRCLPPRKVUDLHSNKIKSVPKQVKLAEQN 479
 QY 413 NDENCSSWEFTVVNNALSYNKLSDSFRCPSKIQDINNNOIQVPKENITHMAIRELN 472
 QY 480 VAENSLTILPGCSFSSLSVLTIONSVHPSAFPSOCOMRSKAGDNPFQCTCELRE 539
 QY 473 IANFLNFTDLPGCSRFSRUSVNINTMNFISPLSDFVQSCORVKTANGRNPFCTELK 532
 Db 540 FVGNIDQVSSEVLEGMPDSYKCYPSYRGSPKDFHMSLSCNTLITVIGATMLVA 599
 Qy 533 FIQ-LETVSEVMWGVWSPSYTCEYFLNLAGTRKDVHLSCTNALLTVIVMLVLG 591
 Db 600 VTVTSLCIVYDLPWYLRMVQWTOPTRRARNIPLELQLRNQFHAFISVEHDSDAWKSE 659
 Qy 592 LAVAFCCLAHDPLWYLRMLGQCTOWHVRVKTQEQLKRNVRFFAHFISTSEHDSLWVNE 651
 Db 660 LVEYLEKED--IOTCLHERNPVCKSIVENIINCCEKSYSIFVUSPNFVQESENHYELY 717
 Qy 652 LPNLEKEBEDSILICLCSYFDPGKSISENIVSFTEKSYSIFVUSPNFVQESENHYFY 711
 Db 718 FAHNLFHGSNNLLILIEPIRONSIPNCKHKLKALMTORTYQOMPKEKSKRGLFWANI 777
 Qy 712 FAHNLFHENDSHDLILLIEPIPYCIPTRYHKULAKLEVLPKORRKCGLFWANL 771
 Db 778 RAJAFNMKJLVTENDVKS 796
 Qy 772 RAJAINVNVLATREMEYLQT 790

RESULT 8

US-09-992-598-57
 Sequence 57, Application US/09992598
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber-Hanspetter
 APPLICANT: Gerritzen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: KJJava, Ivar J.
 APPLICANT: Napior, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C20

CURRENT APPLICATION NUMBER: US/09/992,598
 CURRENT FILING DATE: 2001-11-14
 CURRENT APPLICATION NUMBER: 60/065311
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
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 PRIOR APPLICATION NUMBER: 60/088876

RESULT 9
US-09-989-735-57
Sequence 57, Application US/09989735
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Ferrara, Napoleone
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: KJavvin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Wood, William T.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
FILE REFERENCE: P2730P1C61
CURRENT APPLICATION NUMBER: US/09/989, 735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/089947

QY 660 LVPYLED--IQICLHERNFGKSVIENINICKEYKSIVLULSNPQVSBWCHVELI 717
Db 652 LIPNEKEGDSLILCILYEVSDPGKSISENIVSFIKSYSTIVLSPNVOEWCHEFY 711
QY 718 FAHNLFREGSNNLILILLEP1PONSIRNKYKUKLMQRTYLQWPKEKSRRGFLWANI 777
Db 712 FAHNLFRENSHILILLEP1PFCIPTRYHKLAKALLEKAYLVLPDRRKGFLFWANI 771
QY 778 RAAFMKLTUVTENN DVKS 796
Db 772 RAAINVNLATREMELYOT 790

APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: KJavin, Ivor J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zenlin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P2730PIC60
 CURRENT APPLICATION NUMBER: US/09-1989-726
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 45.9%; Score 1905.5; DB 3; Length 811;
Best Local Similarity 47.8%; Pkd. No. 8.e-174; Mismatches 382; Conservative 145; Indels 21; Gaps 10;

Qy 8 IIVKSEHFFVCLMILIV-GTRIGEDSGNEFAVKSKRGHLHVPKDPLKTKVDMSONYAE 66
Db 3 IIRNITYIFCSTIWTABGDAPPEERBLMTCSNMSLRKVPADLPTATTLDLSNLFO 62
Qy 67 LQVSDDMSFLSLTIVLRLSHNIIQLQDLSVFKNQDIBYLDIHSNQIQKISCHPIVSFRHL 126
Db 63 IQQSDPHSVKLRLVLTCHNQDIFTPFENKELRYLD-SNRKKSVTWYLALRVL 122
Qy 127 DLSFENDPKALPICKERGNGLSQNPLGISAMKQDLPATAHLHSYTLLDQRNNYTKEN 186
Db 123 DLSDNDPDTMICEAGNMHLEILGLSGAKIQKSDFOKIAHLHNTVFLGERT--LPHY 180
Qy 187 ETESLOITLNAKTILHVFHPTLFAIQNISTNLGCQLTNTKLNDNCQPIKESELT 246
Db 181 BEGSLPLINTTCKHTVLPMDTNFWVLLRDGKTKLMTNT---DGKSOPVSY--EMQ 234
Qy 247 RGSTLIM----FTLNHIEETWKCLVRFQMPKPEYLMVNLYNLT---IESIREDFY 299
Db 235 ENLSSLNAKTISVLLNKVDLWDDLELUQFLQWHTSYEHPQRNUTFGKAYLDNSFDY 294
Qy 300 SKTTLKALTIITNOQFLFSOTALYTFESNMMITISOPFIMCPAPSTERFLN 359
Db 295 SNTVMEKITKHVHRVYFIQODKIVLUTKODIENUTISNAQMOPHMLFPVPTKQYLN 354
Qy 360 FTQNUFVDSIIEKSTUVKLERLILOKNGLKDQFLKGJGMTPKMSBILDWSNLSGR 419
Db 355 FANNLTDIDELPHLPHKILILNGNKLTLSLVSCFANTP-LHLDLDSQNLQH-K 412

RESULT 11
US-09-97-514-57
Sequence 57, Application US/09997514
Patent No. 7019116
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyer, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeier
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjavian, Ivar J.
APPLICANT: Napier, Maty A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091C46
CURRENT APPLICATION NUMBER: US/09/97-514
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/09787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770

Qy 420 HKENCTIWESTIWNLSSNMLTDSSYFRCUPRKUDLHSNKKISVPKQVKLALQEIN 479
Db 413 NDENGSSWPEWVNMLSYNLKLSDSYFRCPSKQIQLDANNQQTQVPEKTHWALREIN 472
Db 480 VAFNSLTDQPGGSFSSLSVLTIDNSVSHPSADFFQSOSCKMRSTKAGDNPFQCTCELR 539
Db 473 IAFNFILTDQGCSHSRSRLSUNIENANFILSPSLPVOQSCOEVKILAGRNPNFRTCELN 532
Db 540 FVKNIDOVSSBVLGWPDSYKDYPESYGSPKDFQHMSBLSCTTLLTIVTGATMVLIA 599
Db 533 FIQ-LFTYSEVMVMSDSTCEPLNRLTRIKVHBLSCNTALLAVITIVVIMLV 591
Qy 600 VTTSCLCIVYLDPWYLRMCQWTORRARNIPBLEORNQHAFISTSEHDSAWKSR 659
Db 592 LAVARCCLHFDPBLPWYLRMLQCTQFWHRVRKTQBOQKVRHAFISSEHDSLWVNE 651
Qy 660 IVPYEKKD-IQICLHERNFPVGKSVENIINCEKSYKSFULSPNIVQSENCHYELY 717
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Db 712 FAHNMFHEMSDHITLILRIPPFYCIPTRYKUQKALLEKRAYEWPKDKRKCGFLWANL 771
Qy 778 RAFAFMKLTIVTENNDVKS 796
Db 772 RAININVNLATREMELQT 790


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; PRIOR FILING DATE: 1998-07-01
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; PRIOR APPLICATION NUMBER: 60/091633
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          45.9%; Score 1905.5; DB 3; Length 811;
Best Local Similarity 47.8%; Pred. No. 8.2e-174;
Matches 382; Conservative 145; Mismatches 251; Indels 21; Gaps 10;
Qy
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  3 I R N I Y I F C S I V M T A E G D A P L P E R E B L M T C S N M S L R K V A D L T P A T T I D S N L F Q 62
Qy
  67 I Q V S D M S P L S E L T V R L S H R I Q O L D S V F F N Q D E Y L D I S H N Q L Q K I S C H P I S F R H L 126
  63 I Q S S D P F H S V S K L R V L I T C H N I R Q O L D K T F F N K E L Y D I S N R R K S V W Y L A G L R Y L 122
Qy
  127 D L S F N D F K A L D I C K E F G N L S O N F G I S A M M Q L O D L P I A M L H S Y I L D J R N Y I K E N 186
  123 D L S F N D F D T M P I C E A G M S M E L I G S G A K I Q K S P Q K A H I H U N T V F G F T - L P H Y 180
Qy
  187 E T E S I Q I L N A T H L H V F H P T S I F A O V N I S T N G C L O L T I K L A N D N C O V I K U L S E L T 246
  181 E B G S P I L N T T R K H T V L P M D O I N F W W L I R D G I K T S K I L E M T I N I - - D G K S Q P V S Y - - E M Q 234
Qy
  247 R G S T I L N - - - F T I N H E T T W K C L V R V F O L P K V E Y V I Y N U T I - - E S I R E D F T Y 299
  235 R N L S L E N A K T I S V T L L K V D L W D D L F U L Q F W H T S V E H R O I R V T F G K A Y L D H N S F D Y 294
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  295 S N T V M T K I L E H V H F R V F V I Q D Q K I V L I T D M I N T I S A Q P M I L F P R Y P T F Q Y L N 354
Db
  360 F T O N V E D S T I E K C S T M V K U M P I L L O R G N G L D F K Q G M T I K D M S I E B L D O V S W N S L E S G R 419
  355 P A N N I L T D E L F K R T I O L P H L K T I L I N G N K L E T I S L V C F A M A N T P - L E H D I S Q N L I Q H - K 412
Qy
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  413 N D E N C S W P E T V V N M L S Y N K L S D S V F R C L P K S I Q I L D N N N Q I Q V P K E T H I M A L R E N 472
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Qy
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Qy
  600 V T V T S L C I V I D L P W M V A M C Q T O R R A R I P L E R L O R N I Q H A F T I S Y S H D S A W K S E 659
  592 L A V A F C C L H F D L P W Y L R M L G C O T O W H V R K T O E Q L K R N R F A H T I S Y S H D S L W V K N E 651
Qy
  660 I V P Y L K E D - - I Q I C H E R N I V P G K S T V E N T I N C T E K Y K S I F V I S P N F V O S E C H E L Y 717
  652 L I P N L E K D G S I C L I C Y S P D G K S I S E N T I V S F I R K Y S I F V U L S P N F V O N E C H E F Y 711
Qy
  718 F A H N H L P F H E G N L L I L L E P I Q N S I P N K H K L K A M T Q V Y L O M P K E K K S R G L E W A N T 777
  712 F A H N H L F H E N S D H I L L E P I P F Y C I P T R I H K L K A L L E K A Y L E W P K D R K C G L F W A N L 771
Qy
  778 R A F A N N K L T A T T E N D V K S 796
  772 R A A I N V N L A T R E M Y E L Q T 790

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RESULT 12
US-03-989-728-57
Sequence 57, Application US/09989728
Patent No. 7029873

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Bottstein, David

APPLICANT: Destroyer, Luc

APPLICANT: Batton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanae, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C72

CURRENT APPLICATION NUMBER: US/09/989, 728

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-05-16

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PRIOR FILING DATE: 1997-10-17

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PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088029

APPLICANT: William S. P. Mickey
APPLICANT: Wood, William T.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transferred
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2730/PIC37
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CURRENT FILING DATE: 2001-11-15
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 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Bottstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hans Peter
 ; APPLICANT: Gerritsen, Mary B.
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 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Jr. Christopher
 ; APPLICANT: Hurniak, Michael A.
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: PCT7301PC38
 ; CURRENT APPLICATION NUMBER: US/09/997,653
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; PRIOR FILING DATE: 1998-07-09

Query Match 45.9%; Score 1905.5; DB 3; Length 811;
Best Local Similarity 47.8%; Pred. No. 8.2e-174;
Matches 382; Conservative 145; Mismatches 251; Index 21; Gaps 10;

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67 LVQSMFSLSELTVLURSHRQLDLSVTFKNQDLEYLDISHNQLOKISCH-PIVSRL 126	63 LQSSDFHSVKRVLVILCHNRQQLDLKTFBNKELRYLDLNSRNRLKSUTWLLAGRL 122
127 DISFNDPKALPCKEFGNLSQLNFGLSAMSQKQDULPLRMLHLSYILDRLRNYIKEN 186	181 BEGSLPILNTTKLHTVLPMOTNWVLLRDGKTSKILEMNTI---DGKSOPVSY-EMQ 234
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295 SNTVARTIKLEHHHRVVFYIQQDKIYLLTQDIENTISNAQMPLFLPVPTKQYLN 354	360 FTQNFITDSFEKCSTLVKLTQIQLNGKLDFKGULMKTOMPSBILDYFWSNLSERG 419
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355 FANNLTIDELFKRTIQOLPHKLTLINGKLTLSVCFANNTP-LEHLDLSQNLIQH-K 412	420 HKENTIWESIVLNUMLSSNMLTDYSCRPLRKPRLDHSMKIKSUPKQVNLKAOELN 479
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; GENERAL INFORMATION:	
; APPLICANT: Ashkenazi, Avi J.	
; APPLICANT: Baker, Kevin P.	
; APPLICANT: Batestein, David	
; APPLICANT: Desnoyers, Luc	

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 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zenin
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Job time : 57 secs

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 Listing first 45 summaries

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4	2748.8	99.8	2760	US-09-949-002-100
5	1444.2	52.5	2366	US-09-949-002-65
6	1426.4	51.8	2367	US-09-949-002-236
7	1392	50.6	6392	US-09-949-002-637
8	9	50.6	6392	US-09-949-002-808
9	777.2	28.2	3462	US-09-991-181-56
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11	777.2	28.2	3462	US-09-991-333-56
12	777.2	28.2	3462	US-09-992-598-56
13	777.2	28.2	3462	US-09-998-735-56
14	777.2	28.2	3462	US-09-989-776-56
15	777.2	28.2	3462	US-09-997-514-56
16	777.2	28.2	3462	US-09-989-728-56
17	777.2	28.2	3462	US-09-997-349-56
18	777.2	28.2	3462	US-09-997-653-56
19	777.2	28.2	3462	US-09-989-233A,56
20	600.6	21.8	601	US-09-949-002-3308
21	600.6	21.8	601	US-09-949-002-8228
22	540	19.6	601	US-09-949-002-2394
23	540	19.6	601	US-09-949-002-9241

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Length	DB ID	Description
1	2749.8	99.9	2758	US-09-949-002-226
2	2749.8	99.9	6758	Sequence 226, App
3	2749.8	99.9	6758	Sequence 672, App
4	2748.8	99.8	2760	Sequence 798, App
5	1444.2	52.5	2366	Sequence 100, App
6	1426.4	51.8	2367	Sequence 65, App
7	1392	50.6	6392	Sequence 236, App
8	9	50.6	6392	Sequence 637, App
9	777.2	28.2	3462	Sequence 808, App
10	777.2	28.2	3462	Sequence 56, App
11	777.2	28.2	3462	Sequence 56, App
12	777.2	28.2	3462	Sequence 56, App
13	777.2	28.2	3462	Sequence 56, App
14	777.2	28.2	3462	Sequence 56, App
15	777.2	28.2	3462	Sequence 56, App
16	777.2	28.2	3462	Sequence 56, App
17	777.2	28.2	3462	Sequence 56, App
18	777.2	28.2	3462	Sequence 56, App
19	777.2	28.2	3462	Sequence 56, App
20	600.6	21.8	601	Sequence 3378, App
21	600.6	21.8	601	Sequence 8628, App
22	540	19.6	601	Sequence 2394, App
23	540	19.6	601	Sequence 9241, App

RESULTS

result No.	Score	Query Length	DB ID	Description
1	2749.8	99.9	2758	US-09-949-002-226
2	2749.8	99.9	6758	Sequence 226, Application US/09949002
3	2749.8	99.9	6758	Patent No. 6900016
4	2748.8	99.8	2760	GENERAL INFORMATION:
5	1444.2	52.5	2366	APPLICANT: VENTER, J. Craig et al.
6	1426.4	51.8	2367	TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION, AND USES THEREOF
7	9	50.6	6392	FILE REFERENCE: CLO00790
8	9	50.6	6392	CURRENT APPLICATION NUMBER: US/09-949,002
9	9	50.6	6392	CURRENT FILING DATE: 2000-01-28
10	10	50.6	6392	PRIOR APPLICATION NUMBER: 60/231,401
c	43	61.2	3220	NUMBER OF SEQ ID NOS: 10823
c	44	61.2	3220	SOFTWARE: FASTSEQ for Windows Version 4.0
c	45	56.6	31141	SEQ ID NO: 226
i				LENGTH: 2758
i				TYPE: DNA
i				ORGANISM: Human
i				US-09-949-002-226

ALIGNMENTS

Query	Match	Similarity	Score	DB	Length
1 AGTATTGGACTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	1	99.9%	2749.8	3	2758;
2 AGATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	2	99.9%	2749.8	3	2758;
3 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	3	99.9%	6758	3	6758;
4 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	4	99.9%	6758	3	6758;
5 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	5	99.9%	6758	3	6758;
6 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	6	99.9%	6758	3	6758;
7 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	7	99.9%	6392	3	6392;
8 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	8	99.9%	6392	3	6392;
9 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	9	99.9%	6392	3	6392;
10 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	10	99.9%	6392	3	6392;
11 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	11	99.9%	6392	3	6392;
12 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	12	99.9%	6392	3	6392;
13 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	13	99.9%	6392	3	6392;
14 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	14	99.9%	6392	3	6392;
15 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	15	99.9%	6392	3	6392;
16 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	16	99.9%	6392	3	6392;
17 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	17	99.9%	6392	3	6392;
18 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	18	99.9%	6392	3	6392;
19 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	19	99.9%	6392	3	6392;
20 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	20	99.9%	6392	3	6392;
21 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	21	99.9%	6392	3	6392;
22 AGTATTGGACCTATCATGAGATGCTCTGAAGAGAACACCCTTAGATACTGC	22	99.9%	6392	3	6392;

QY 301 ACGATTTGACACTTCCCATACAGATCAGCTACTGGTTAAGTGTTCAGTC 360
Db 302 ACAGTTTGACACTTCCCATACAGATCAGCTACTGGTTAAGTGTTCAGTC 361
QY 361 AACAGAGATTAGAATTTGAGATTCTTAATAGTCCAAGATTCCTCCAT 420
Db 362 AACAGAGATTAGAATTTGAGATTCTTAATAGTCCAAGATTCCTCCAT 421
QY 421 CCTATGTTGAGTTTCAGGCATTAGATCTCTCAAGGCTTGCCAT 480
Db 422 CCTATGTTGAGTTTCAGGCATTAGATCTCTCAAGGCTTGCCAT 481
QY 481 TGTAAAGGAATTGGCACTTACACACTGAACTTCCTGGATGGAGCTG 540
Db 482 TGTAAAGGAATTGGCACTTACACACTGAACTTCCTGGATGGAGCTG 541
QY 541 CAAAATAGATTGCTGCCATTGTCACITGCATCTAATGTCATAAAGAT 600
Db 542 CAAAATAGATTGCTGCCATTGTCACITGCATCTAATGTCATAAAGAT 601
QY 601 AGAAATTATAAAGAAATGAGACAGAAAGTCAAAATTCTGAATGCAAACC 660
Db 602 AGAAATTATAAAGAAATGAGACAGAAAGTCAAAATTCTGAATGCAAACC 661
QY 661 CTTCACTTGTGTTTCCCACACTAGTTATGGTATCCAGTGACATTCAGTTAAT 720
Db 662 CTTCACTTGTGTTTCCCACACTAGTTATGGTATCCAGTGACATTCAGTTAAT 721
QY 721 ACTTTAGGTGTTAACACTGACTAATTAATGATGATGACACTGCAATTTC 780
Db 722 ACTTTAGGTGTTAACACTGACTAATTAATGATGATGACACTGCAATTTC 781
QY 781 ATTAATTTATCAGACTCCAGGTTAACCTACTGATTTACCTCAACC 840
Db 782 ATTAATTTATCAGACTCCAGGTTAACCTACTGATTTACCTCAACC 841
QY 841 ATAGAACGACGTTGGAAATGCGTGTGAGAATCTTCAATTCTTGGCCAAACCTGT 900
Db 842 ATAGAACGACGTTGGAAATGCGTGTGAGAATCTTGGCCAAACCTGT 901
QY 901 GATATCTCAATTACATTACATTAATGAGACATCTGTTGAGAGATTCT 960
Db 902 GATATCTCAATTACATTACATTAATGAGACATCTGTTGAGAGATTCT 961
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Db 962 TATTCAAACGACATGAGATTGACATAGAACATACAGAACCAATTCTG 1021
QY 1021 TTTCAGACAGCAGCTTGTGAGATGACATTGATGTTAACCT 1080
Db 1022 TTTCAGACAGCAGCTTGTGAGATGACATTGATGTTAACCT 1081
QY 1081 TCAGATCACCTTTATACATGCTGTTCTGACCAAGACATTAAGTTG 1140
Db 1082 TCAGATCACCTTTATACATGCTGTTCTGACCAAGACATTAAGTTG 1141
QY 1141 AACTTACCCAGACGTTTCAGATGATTTGAAAGTTCACCTTAGTAA 1200
Db 1142 AACTTACCCAGACGTTTCAGATGATTTGAAAGTTCACCTTAGTAA 1201
QY 1201 TTGGAGACACTTACCTACAAAAAATGGTAAAGACCTTTCAAGTGGCTCATG 1260
Db 1202 TTGGAGACACTTACCTACAAAAAATGGTAAAGACCTTTCAAGTGGCTCATG 1261
QY 1261 AGGAAGATAGTCCTCTTGAATCTGAGTTGAGCTGAAATCTTGGTAACT 1320
Db 1262 AGGAAGATAGTCCTCTTGAATCTGAGTTGAGCTGAAATCTTGGTAACT 1321
QY 1321 AGACATAAGAAACTGACTTGGTCAAGTGGTAAATTCTCTCAAT 1380
Db 1322 AGACATAAGAAACTGACTTGGTCAAGTGGTAAATTCTCTCAAT 1381
QY 1381 ATGCTTACTGACTCTGTTAGATGTTACCTCCAGGATCAAGGACTGAC 1440

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Db 1442 AGCAATAAAATAAGGCGTCTAACAGTGTAAACTGGAGCTTGCAGAAC 1501
QY 1501 ATGTTCTCACTTAACTGACCTCTGATGGCAGTTAGCAGCTTCT 1560
Db 1502 ATGTTCTCACTTAACTTAACTGACCTCTGATGGCAGCTTCT 1561
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QY 1861 GCTGTCAGTGTGACCTCCCTGATCTACTTGATCTGCCCTGTTCTCAGGATG 1920
Db 1862 GCTGTCAGTGTGACCTCCCTGATCTACTTGATCTGCCCTGTTCTCAGGATG 1921
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Db 1922 TGCCAGTGGACCACTCGGGCGAGGCGACATACCTTAGAGAAACTCCAAGA 1981
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Db 2042 GATTGTCACCTACTGAGAAAAGAGATATCAGATGTTCTCATGAGGACTT 2101
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Db 2102 GTCCCTGGACAGGTTCTGGAATATCTCACTGATGAGAACTTCAAGTCC 2161
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Db 2162 ATCTTGTGTTGTCCTCCAACTTGTGTCAGAGTGGGCCATTAGGAGACTT 2221
QY 2221 GCCCATACAATCTCTCATGAGATCTAACTTCACTTACTGAAACC 2280
Db 2222 GCCCATACAATCTCTCATGAGATCTAACTTCACTTACTGAAACC 2281
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QY 2341 ACTTATGTCAGTGGCCCAAGGAGAAAGAACACGCGGGCTTGGCTACCTAGA 2400
Db 2342 ACTTATGTCAGTGGCCCAAGGAGAAAGAACACGCGGGCTTGGCTACCTAGA 2401
QY 2401 GCGCTTAAATGAAATTACACTGACATGTCAGTGAATCTTAA 2460
Db 2402 GCGCTTAAATGAAATTACACTGACATGTCAGTGAATCTTAA 2461
QY 2461 ATTTAGAACTTAACTAGAACCAATTACTTCTGATGAGTGTACACT 2520

Db 2462 ATTTAGGAATTCACTAGAACCTTATTACTTGTGATGGTGAATGACGT 2521
 Qy 2521 CGTAAGTAACTGCTCGAGGTCCTCAATTCTCATGCCTCAGAACCTTACA 2580
 Db 2522 CTTAAGTAACTGCTCGAGGTCCTCAATTCTCATGCCTCAGAACCTTACA 2581
 Qy 2581 AACAAATGTTCATCTGGGACTGAGCTAGCGGTAGGGTAGCTGGCCATTAGAC 2640
 Db 2582 AACAAATGTTCATCTGGGACTGAGCTAGCGGTAGGGTAGCTGGCCATTAGAC 2641
 Qy 2641 AGCCCAGTCTCTGGTTAACATTATGTTCAATGAAAGACGTCCTTGAGTAA 2700
 Db 2642 AGCCAGTCTCTGGTTAACATTATGTTCAATGAAAGACGTCCTTGAGTAA 2701
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 RESULT 2
 US-09-949-002-672
 ; Sequence 672, Application US/09949002
 ; Patent No. 6990016
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
 ; FILE REFERENCE: C1000790
 ; CURRENT APPLICATION NUMBER: US/09-949, 002
 ; CURRENT FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/231,401
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 10823
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 672
 ; LENGTH: 6758
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-002-672
 Query Match 99.9%; Score 2749; DB 3; Length 6758;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Gaps 0;
 Matches 2751; Conservative 0; Indels 0;
 Qy 1 AGAATTGGACTCATCAAGATGCTGAAGAGAACACCTTGTAGATAGCCACTGC 60
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 Qy 61 AACATCATGACAAAGAACGAAACCTTGTAAAGCTTCATTGTTGCTTATG 120
 Db 2062 AACATCATGACAAAGAACGAAACCTTGTAAAGCTTCATTGTTGCTTATG 2121
 Qy 121 ATCATAATAGTTGACCGAGATCCTCGAGGAAATGAAATTGAGTACAAG 180
 Db 2122 ATCATATAGTTGACCGAGATCCTCGAGGAAATGAAATTGAGTACAAG 2181
 Qy 181 TCAAAGAGGCTTATCATGTTCCAAGAACCTACCGCTGAAGAACGCTTAGAT 240
 Db 2182 TCAAAGAGGCTTATCATGTTCCAAGAACCTACCGCTGAAGAACGCTTAGAT 2241
 Qy 241 ATGCTCAGAACTACATCGCTGAGCTTCAGGCTCTGACATGAGCTTCATCAGGTG 300
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 Qy 301 ACAGTTTGACACTTCCATACAGATCACTGACTCTGTTAAGTGTTCAGTC 360
 Db 2302 ACAGTTTGACACTTCCATACAGATCACTGACTCTGTTAAGTGTTCAGTC 361
 Qy 361 AACAGGAGTTAGAAATTGAGTTATCTAATCAGTGCAGAAAGATTCCTGCCAT 420
 Db 2362 AACAGGAGTTAGAAATTGAGTTATCTAATCAGTGCAGAAAGATTCCTGCCAT 2421
 Qy 421 CCTATTGAGTTGCGCATTTAGCTCTCATGATTCAGGCTGCCATC 480
 Db 2422 CCTATTGAGTTGCGCATTTAGCTCTCATGATTCAGGCTGCCATC 2481
 Qy 481 TCTAAGGAATTGGCACTTACACTGATGATTGCGATTGAGTCATGAGCTG 540
 Db 2482 TGTAAAGGATTGGCACTTACACTGATGATTGCGATTGAGTCATGAGCTG 2541
 Qy 541 CAAAAATTGATTGCGCATTTGCACTGACTGCACTGATCTAATCCTCTGGATT 600
 Db 2542 CAAAAATTGATTGCGCATTTGCACTGACTGATCTAATCCTCTGGATT 2601
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 Qy 661 CTTCACCTGTTGTTACCCACTACTTTATGCTGTATCCAGTGAACATTCAGTAA 720
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 Qy 781 ATTAATTTTATCAGACTACCCAGGTTCAACCTACTGAAATTACCTCACCAC 840
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 Qy 841 ATAGAAAGCAGTGGAAATGCGCTGGTAGACTCTTCAATTCTGGCCAAACCTGTG 900
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 Db 2902 GAATATCTCAATTATCACAATTAACTTACGATGACATAGAACATTCACGAACTGTTCTG 2961
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 Db 2962 TATCPAAAGACATGACATAGAACATAGAACATTCACGAACTGTTCTG 3021
 Qy 1021 TTTTCAAGACAGCTTGTACACCGTTCTGAGATGACATATGAGTTAACATT 1080
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 Qy 1081 TCAGATACACCTTTATACATGCTGTTGCTCATGCACAAACATCAAGTTTC 1140
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 Qy 1141 AACTTACCCAGAACGTTTCAGAGTAAATTGAAATGTCACGTTGTTAA 1200
 Db 3142 AACTTACCCAGAACGTTTCAGAGTAAATTGAAATGTCACGTTGTTAA 3201
 Qy 1201 TTGGAGACACTATCTACAAAAAATGGTTAAAGACCTTCAAAAGTAGTGTCTAG 1260
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 Qy 1261 ACAGAAGGATATGCGCTCTTGGAAATATCGATGCTGCGAAATTCCTGGAACTCTGG 1320
 Db 3262 ACAGAAGGATATGCGCTCTTGGAAATATCGATGCTGCGAAATTCCTGG 3321
 Qy 1321 AGACATAAGAACCTGACTTGGGTAGAGTAACTGGTAAATGTCCTCAAT 1380
 Db 3322 AGACATAAGAACCTGACTTGGGTAGAGTAACTGGTAAATGTCCTCAAT 3381
 Qy 1381 ATGCTTACGACTCTGTTCAAGTGTAACTCCAGGATCAAGGACTGATCTTCAC 1440
 Db 3382 ATGCTTACGACTCTGTTCAAGTGTAACTCCAGGATCAAGGACTGATCTTCAC 3441
 Qy 1441 AGCAATAATAAGAACGCGTCTCAAACAGTCGAAACTGGAGCTTGCAAGACRC 1500
 Db 3442 AGCAATAATAAGAACGCGTCTCAAACAGTCGAAACTGGAGCTTGCAAGACRC 3501
 Qy 1501 ATGCTGCTTCAATTCTTAACTGACCTCTGGATGCGCAGTTAGCAGCCTCT 1560

Db 3502 ATATGTTGCTTCATTCATTACTGACCTTCTGGAGTGGCAGCTTAGAGGCCTCT 3561
 Qy 1561 GATTTGATCATGATECAATTCAGTTCCACCCATCGGTGATTCTTCAGAGCTC 1620
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 Db 3622 CAGAAGATGAGGTCAATAAGCAGGGACATCCATCCATGACTGTGAGCTAAGA 3681
 Qy 1681 GATTTGTCAAATAATAGACAGAAGTCAAGTGAGTGAAGTGTAGAGGCTGCCCTGATCT 1740
 Db 3682 GATTTGTCAAATAATAGACAGAAGTCAAGTGAGTGAAGTGTAGAGGCTGCCCTGATCT 3741
 Qy 1741 TATAAGTGTGACTACCCAGAAGTTAGAGGAAGCCACTAAGCTTACAGTCT 1800
 Db 3742 TATAAGTGTGACTACCCAGAAGTTAGAGGAAGCCACTAAGCTTACAGTCT 3801
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 3802 GAATATCCTGACATACTGTCATGTCACCATGGTCCACCATCTGGGTG 3861
 Qy 1861 GCTGTGACTGTGACCTCCTGTCATCTACTGTGAGTCTGAGGTTG 1920
 3862 GCTGTGACTGTGACCTCCTGTCATCTACTGTGAGTCTGAGGTTG 3921
 1921 TCCCACTGAGAACAGACTCGGGCAGGGCGAACATACCCCTAGAAGCTCCAAGA 1980
 Qy 3922 TCCCACTGAGAACAGACTCGGGCAGGGCGAACATACCCCTAGAAGCTCCAAGA 3981
 Db 1981 AACCTCCAGTTCACTGTTATTCTATAGACATGATCTGCTGGCTGAAAGT 2040
 Db 3982 AACCTCCAGTTCACTGTTATTCTATAGACATGATCTGCTGGCTGAAAGT 4041
 Qy 2041 GATTTGTTACCTTACCTAGAAAGAAGATATCACAGATTCTTCATGAGGAACTT 2100
 Db 4042 GATTTGTTACCTTACCTAGAAAGAAGATATCACAGATTCTTCATGAGGAACTT 4101
 2101 GTCCCCGGCAAGAGCATGTGAGAAATATCACAGATTCTTCATGAGGAACTT 2160
 Db 4102 GTCCTCTGGCAAGAGCATGTGAGAAATATCACAGATTCTTCATGAGGAACTT 4161
 2161 ATCTTGTGTTCTCCAACTTGTCCAGGTGAGTGGTCCATTAGACTCTATT 2220
 Db 4162 ATCTTGTGTTCTCCAACTTGTCCAGGTGAGTGGTCCATTAGACTCTATT 4221
 Qy 2221 GCCCATACAACATCTTCATGAGGATCTATACITAATCTCACTTCTGAAACC 2280
 Db 4222 GCCCATACAACATCTTCATGAGGATCTATACITAATCTCACTTCTGAAACC 4281
 Qy 2281 ATTCCACAGAACGATTCACCAACAGTACACAACTGAGGTCTACCGAGGG 2340
 Db 4282 ATTCCACAGAACGATTCACCAACAGTACACAACTGAGGTCTACCGAGGG 4341
 2341 ACTTATTCGCGTGGCCAAGGAGAACGAAACGCGGGCTTTRGGCTACATTAGA 2400
 Db 4342 ACTTATTCGCGTGGCCAAGGAGAACGAAACGCGGGCTTTRGGCTACATTAGA 4401
 Qy 2401 GCGCTTTAAATGAATTAACACTAGTCACTGAAACAAAGTGTGAAACTTAAA 2460
 Db 4402 GCGCTTTAAATGAATTAACACTAGTCACTGAAACAAAGTGTGAAACTTAAA 4461
 Qy 2461 ATTTAGGAATTCACCTAGAAACCAATTACTTACTGTGAGTGTGAAACTTAAA 2520
 Db 4462 ATTTAGGAATTCACCTAGAAACCAATTACTTACTGTGAGTGTGAAACTTAAA 4521
 2521 CGTAACTGAACTCTGGGGACTGAGCTGAGGCTGGGTAGGTAGCCGTTGAGAC 2580
 Db 4522 CGTAACTGAACTCTGGGGACTGAGCTGAGGCTGGGTAGGTAGCCGTTGAGAC 4581
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RESULT 3
 US-09-949-002-798
 Sequence 798, Application US/09949002
 ; Patent No. 690016
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CL000790
 ; CURRENT APPLICATION NUMBER: US/09/0949, 002
 ; CURRENT FILING DATE: 2000-01-28
 ; PRIORITY APPLICATION NUMBER: 60/231, 401
 ; PRIORITY FILING DATE: 2000-03-08
 ; NUMBER OF SEQ ID NOS: 10823
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 798
 ; LENGTH: 6758
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-002-798

Query Match 99.9%; Score 2749.8; DB 3; Length 6758;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;
 Matches 2751; Conservative 0;

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Qy 181 TCAAAGAGAGCTCTATCATGTTCCAAGAACCTACCGCTGAAACAAAGCTTAGAT 240	Db 2182 TCAAAGAGAGCTCTATCATGTTCCAAGAACCTACCGCTGAAACAAAGCTTAGAT 2241
Qy 241 ATGTCAGAACACTCTGGTGTGAGCTTCAAGCTCTGACTGTGAGCTTCTATCAGAGTC 300	Db 2242 ATGTCAGAACACTCTGGTGTGAGCTTCAAGCTCTGACTGTGAGCTTCTATCAGAGTC 2301
Qy 301 ACAGTTGTGAGCTTCCATACAGATCAGCTACTGATTAAGTGTGTTCAAGTC 360	Db 2302 ACAGTTGTGAGCTTCCATACAGATCAGCTACTGATTAAGTGTGTTCAAGTC 2361
Qy 361 AACAGGAGTTAGAATTTGGATTATCTCATTAATCAGTGTGAAAGATATCCGTCAT 420	Db 2362 AACAGGAGTTAGAATTTGGATTATCTCATTAATCAGTGTGAAAGATATCCGTCAT 2421
Qy 421 CCTATGTGAGCTTCCATACAGATCAGCTACTGATTAAGTGTGTTCAAGTC 480	Db 2422 CCTATGTGAGCTTCCATACAGATCAGCTACTGATTAAGTGTGTTCAAGTC 2481
Qy 481 TCTAAGGAATTGGCAACTTACATGAACTGATGTTGAGTGTGAGCTGATGAGCTG 540	Db 2482 TCTAAGGAATTGGCAACTTACATGAACTGATGTTGAGTGTGAGCTGATGAGCTG 2541

QY 541 CAAATATTAGTTGCTGCCAATGTCACATGCATCAAGTATCCCTCTGGATTA 600 Db 3622 CAGAAGTAGGTCAAATAAGCAGGGACATCCATTCCHATGTRACTGAGCTAGA 3681
Db 2542 CAAATATTAGTTGCTGCCAATGTCACATGCATCAAGTATCCCTCTGGATTA 2601 QY 1681 GAATTGTCAAAATTTAGCCAAGTATCAGTGAAGTTAGGGCTGGCTGATCT 1740
QY 601 AGAAATTATATAAAAGAAATGAGACAGAAAGTCAAAATTGAAATGCAAACC 660 Db 3682 GAATTGTCAAAATTTAGCCAAGTATCAGTGAAGTGTAGGGCTGGCTGATCT 3741
Db 2602 AGAAATTATATAAAAGAAATGAGACAGAAAGTCAAAATTGAAATGCAAACC 2661 QY 1741 TATAAGTGACTACCCAGAAAGTTAGAGGAAGGCCACTAACAGTCAGTGAAGTGTAGGGCTGGCTGATCT 1800
QY 661 CTTCACCTGTTTGCACCAACTAGTTATGGTATCCAGTGAACATTCAGTAAT 720 Db 3742 TATAAGTGACTACCCAGAAAGTATGAGGAAGGCCACTAACAGTCAAGTGAACATTCAGTGA 3801
Db 2662 CTTCACCTGTTTGCACCAACTAGTTATGGTATCCAGTGAACATTCAGTGA 2721 QY 1801 GAATTATTTATCAGAACTTACCACTAACCTACTGAACTGTCAGTT 780 Db 3802 GAATTATCTGCAACATTAACHTGCGATCCTCACCATCGTGCACACATGCTG 3861
Db 2722 ACTTGGGCTTCACTACTGAACTTACCACTAACCTACTGAACTGTCAGTT 720 Db 3922 TCCAGTGGACAGCTCGGCCAGGGCCAGGAATACCCCTGCACTACTGGATCTGGCCAAACCTGTG 2901 QY 1861 GCTGTCAGTGTACTCCCTCTGCATCACTACTTGGATCTGGCTGGTACTCAGGATGTG 1920
QY 781 ATTAATTTATCAGAACTTACCACTAACCTACTGAACTGTCAGTT 840 Db 3862 GCTGTCAGTGTACTCCCTCTGCATCACTACTGGATCTGGCTGGTACTCAGGATGTG 3921
Db 2782 ATTAATTTATCAGAACTTACCACTAACCTACTGAACTGTCAGTT 2841 QY 1921 TCCAGTGGACCCAGACTCGGCCAGGGCCAGGAATACCCCTAGAGAAAG 1980
QY 841 ATAGAACAGATTTGGAATGCTGTCAGAACTTACCACTAACCTGTG 900 Db 3982 AACCTCCAGTTCTGTCAGTGTACTCCCTCTGCATCACTACTGGATCTGGTAAAGA 3981
Db 2842 ATAGAACAGATTTGGAATGCTGTCAGAAGCTTCAATTCTTGGCCAAACCTGTG 2901 QY 1981 AACCTCCAGTTCTGTCAGTGTACTCCCTCTGCATCACTACTGGATCTGGTAAAGA 2040
QY 901 GAATATCTCAATTACAACTAACATAATGAAAGCATCTGTGAGAGATTACT 960 Db 3982 AACCTCCAGTTCTGTCAGTGTACTCCCTCTGCATCACTACTGGATCTGGTAAAGA 4041
Db 2902 GAATATCTCAATTACAACTAACATAATGAAAGCATCTGTGAGAGATTACT 2961 QY 2041 GAATGGTACCTTACCTAGAAAGAGATAAACAGATTAACAGATGTCCTCATGAGGAACTT 2100
QY 961 TATTCTAAACGACATGAAAGCATGAACTAACATAATGAAAGCATCTGTGAGAGATTACT 1020 Db 4042 GAATGGTACCTTACCTAGAAAGAGATAAACAGATTAACAGATGTCCTCATGAGGAACTT 4101
Db 2962 TATTCTAAACGACATGAAAGCATGAACTAACATAATGAAAGCATCTGTGAGAGATTACT 3021 QY 2101 GRCCTTGGCAAGAGCATGTGAAATATCATCAACTGCATGAGTACATGTCCTGGTAAAGA 1980
QY 1021 TTTTACAGACAGACTGTTACACGGTTTCTGAGATGACATTGATGTTAACCT 1080 Db 4102 GTCCTCTGGACAGATGTGAAATATCATCAACTGCATGAGTACATGTCCTGGTAAAGA 4161
Db 3082 TTTCACAGACAGACTGTTACACGGTTTCTGAGATGACATTGATGTTAACCT 3081 QY 2161 ATCTTGTGTTGCTCCAACTTGTGCAAGTGAAGTGTGTTGCTGCAATTGAACTPATT 2220
QY 1141 ACTTTACCCAGAACGGTTTACAGATGATGTTGAAATGTTGCAACCTAGTTAA 1200 Db 4162 ATCTTGTGTTGCTCCAACTTGTGCAAGTGTGTTGCTGCAATTGAACTPATT 4221
Db 3142 ACTTTACCCAGAACGGTTTACAGATGATGTTGAAATGTTGCAACCTAGTTAA 3201 QY 2221 GCCCATACAATCTCTCATGAAAGCTAAACTTACTTCACTTACTGGAAACC 2280
Db 1201 TTGGACACACTTACAAAGAAAGATGATGAAAGACCTTCAAGTGGTCTCATG 1260 Db 4222 GCCCATACAATCTCTCATGAAAGCTAAACTTACTTCACTTACTGGAAACC 4281
Db 3202 TTGGACACACTTACAAAGAAAGATGATGAAAGACCTTCAAGTGGTCTCATG 3261 QY 2341 ACTTATGGTGGCCAAAGGAGAAAGAACCTGGCTTGGGTAACTTCTGAGTAA 2400
QY 1261 ACAGAGATATCCCTCTTGGAAATRACTGGATGTTAGCTGAACTTCTGATCTG 1320 Db 4342 ACTTATGGTGGCCAAAGGAGAAAGAACCTGGCTTGGGTAACTTCTGAGTAA 4401
Db 3262 ACAGAGATATGGCTCTTGGAAATRACTGGATGTTAGCTGAACTTCTGAGTAA 3321 Db 4282 ATTCCAGAACAGATTCCTCAACAGTACCAACAGTACCAACAGTGGCTCTCATGCGCG 4341
Db 3322 AGACATAAGAAACTGCACTGGGTGAGAGATAGTGGTTAAATTGCTCAAT 1380 QY 2401 GCGCCTTTAATGAAATTACACTGACTGAAACATGTTGAAATCTTAA 2460
Db 1321 AGACATAAGAAACTGCACTGGGTGAGAGATAGTGGTTAAATTGCTCAAT 1380 Db 4402 GCGCCTTTAATGAAATTACACTGACTGAAACATGTTGAAATCTTAA 4461
Db 3322 AGACATAAGAAACTGCACTGGGTGAGAGATAGTGGTTAAATTGCTCAAT 3381 QY 2461 AATTAGAAATTCAACTTAAAGAAACCAATTACTGGATGTTGAAATGAGCT 2520
QY 1381 ATGCTTACTGACTCTTCTGAGTTACTCTCCAGGAGCAAGTGGCTTGGCTC 1440 Db 4462 AATTAGAAATTCAACTTAAAGAAACCAATTACTGGATGTTGAAATGAGCT 4521
Db 3382 ATGCTTACTGACTCTTCTGAGTTACTCTCCAGGAGCAAGTGGCTTGGCTC 3441 QY 2521 CGTAAGTACTGCTGGAGGTGGCTTCAATTCTGATGCTCTGGAGACTTACAA 2580
Db 1441 AGCAATAAATTAAGGGCTTCTAAACAGCTGAAACTGGAACTTCTGAAACTC 1500 Db 4522 CGTAAGTACTGCTGGAGGTGGCTTCAATTCTGATGCTCTGGAGACTTACAA 4581
Db 3442 AGCAATAAATTAAGGGCTTCTAAACAGCTGAAACTGGAACTTCTGAAACTC 3501 QY 2581 AACATGTTCTCATGGGAACTGAGCTGGCTGAGTGGCTGAGTGGCTGAGAC 2640
QY 1501 ATGTTGCTTCAATTCTTACTGACTCTCTGGATGTTGCGAGCTTGGCTTGGCT 1560 Db 4582 AACATGTTCTCATGGGAACTGAGCTGGCTGAGTGGCTGAGAC 4641
Db 3502 ATGTTGCTTCAATTCTTACTGACTCTCTGGATGTTGCGAGCTTGGCTTGGCT 3561 QY 2641 AGCCAGTCCTCTGGTTATCATTAGTCAATTGAAAGCTCTTCTGAGTAA 2700
QY 1561 GATTTGATCATGTCATGCACTTCAATTGAGCTTCTGGCTTGGCTTGGCT 1620 Db 4642 AGCCAGTCCTCTGGTTATCATTGAAAGCTCTTCTGAGTAA 4701
Db 3562 GATTTGATCATGTCATGCACTTCAATTGAGCTTCTGGCTTGGCTTGGCT 3621 QY 2701 ATGCTGTTCTGAGCTTCAATTGAGCTTCTGGCTTGGCTTGGCTTGGCT 2753

RESULT 4
US-09-949-002-100
Sequence 100, Application US/0949002
; Sequence 100, Application US/0949002
; Patent No. 690016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949, 002
PRIORITY FILING DATE: 2000-01-28
PRIORITY APPLICATION NUMBER: 60/231, 401.
NUMBER OF SEQ ID NOS: 10823
FEATURE:
NAME/KEY: misc_feature
SEQ ID NO: 100
LENGTH: 2760
TYPE: DNA
ORGANISM: Human
OTHER INFORMATION: n = A,T,C or G
US-09-949-002-100

Query Match	Score	Length
Best Local Similarity	99.8%	2748.8
Matches	2750;	DB 3;
Conservative	99.9%	Length 2760;
	Pred. No. 0;	
Mismatches	0;	
Indels	3;	
Gaps	0;	
QY	1	AGAATTGGACTCATTACAGATGCTCTGAAGAAACACCCCTTAGGATAGCCACTGC
Db	2	AGAATTGGACTCATTACAGATGCTCTGAAGAAACACCCCTTAGGATAGCCACTGC
QY	61	AACATCATGACCAAGACAAGAACCTATGTAAAGCTCCATTGTTGSCCTTATG
Db	62	AACATCATGACCAAGACAAGAACCTATGTAAAGCTCCATTGTTGSCCTTATG
QY	121	ATCATAATGTTGACCAAGATCAGTTCGGAGGAATGATTGCACTGAGACAG
Db	122	ATCATAATGTTGACCAAGATCAGTTCGGAGGAATGATTGCACTGAGACAG
QY	181	TCAAAGAGGTCTTATCATGTCCAAAGACCTACCGTCTCCAGGAAATGATTGCACTGAGACAG
Db	182	TCAAAGAGGTCTTATCATGTCCAAAGACCTACCGTCTCCAGGAAATGATTGCACTGAGACAG
QY	241	ATGTCAGRACTACATCGCTGACGTTCACTTGACATGAGCTTCTATCAGAGTG
Db	242	ATGTCAGRACTACATCGCTGAGGTCTCACTTGACATGAGCTTCTATCAGAGTG
QY	301	ACGTTTGAGACTTCCATAACGAAACCGTACTGATTAAGTGTTCAGTC
Db	302	ACGTTTGAGACTTCCATAACGAAACCGTACTGATTAAGTGTTCAGTC
QY	361	AACGGGATTGAGATATTGGATTAICTCATACAGTGCAGAATCTGCCAT
Db	362	AACGGGATTGAGATATTGGATTAICTCATACAGTGCAGAATCTGCCAT
QY	421	CCTATGTGAGTTCAGGCTTACATCATGATTCAGGCTCTGCCAT
Db	422	CCTATGTGAGTTCAGGCTTACATCATGATTCAGGCTCTGCCAT
QY	481	TGTTAGGAATTGCAACTTACACACTGATTCGGATGAGCTGAGCTG
Db	482	TGTTAGGAATTGCAACTTACACACTGATTCGGATGAGCTG
QY	541	CAAAATTAGATTCTGCCAATCTCACTTGCTCAAGTATACTCTGGATT
Db	542	CAAAATTAGATTCTGCCAATCTCACTTGCTCAAGTATACTCTGGATT

Query Match

Score 2748.8; DB 3; Length 2760;

Best Local Similarity 99.8%; Score 2748.8; DB 3; Length 2760;

Matches 2750; Conservative 99.9%; Pred. No. 0;

Mismatches 0; Indels 3; Gaps 0;

QY 1 AGAATTGGACTCATTACAGATGCTCTGAAGAAACACCCCTTAGGATAGCCACTGC 60

Db 2 AGAATTGGACTCATTACAGATGCTCTGAAGAAACACCCCTTAGGATAGCCACTGC 61

QY 61 AACATCATGACCAAGACAAGAACCTATGTAAAGCTCCATTGTTGSCCTTATG 120

Db 62 AACATCATGACCAAGACAAGAACCTATGTAAAGCTCCATTGTTGSCCTTATG 121

QY 121 ATCATAATGTTGACCAAGATCAGTTCGGAGGAATGATTGCACTGAGACAG 180

Db 122 ATCATAATGTTGACCAAGATCAGTTCGGAGGAATGATTGCACTGAGACAG 181

QY 181 TCAAAGAGGTCTTATCATGTCCAAAGACCTACCGTCTCCAGGAAATGATTGCACTGAGACAG 240

Db 182 TCAAAGAGGTCTTATCATGTCCAAAGACCTACCGTCTCCAGGAAATGATTGCACTGAGACAG 241

QY 241 ATGTCAGRACTACATCGCTGACGTTCACTTGACATGAGCTTCTATCAGAGTG 300

Db 242 ATGTCAGRACTACATCGCTGAGGTCTCACTTGACATGAGCTTCTATCAGAGTG 301

QY 301 ACGTTTGAGACTTCCATAACGAAACCGTACTGATTAAGTGTTCAGTC 360

Db 302 ACGTTTGAGACTTCCATAACGAAACCGTACTGATTAAGTGTTCAGTC 361

QY 361 AACGGGATTGAGATATTGGATTAICTCATACAGTGCAGAATCTGCCAT 420

Db 362 AACGGGATTGAGATATTGGATTAICTCATACAGTGCAGAATCTGCCAT 421

QY 421 CCTATGTGAGTTCAGGCTTACATCATGATTCAGGCTCTGCCAT 480

Db 422 CCTATGTGAGTTCAGGCTTACATCATGATTCAGGCTCTGCCAT 481

QY 481 TGTTAGGAATTGCAACTTACACACTGATTCGGATGAGCTGAGCTG 540

Db 482 TGTTAGGAATTGCAACTTACACACTGATTCGGATGAGCTG 541

QY 541 CAAAATTAGATTCTGCCAATCTCACTTGCTCAAGTATACTCTGGATT 600

Db 542 CAAAATTAGATTCTGCCAATCTCACTTGCTCAAGTATACTCTGGATT 601

QY 601 AGAATTATTATAAAGAAATGAGCAGAATGAGCAGAATCTGATGCAAAC

Db 602 AGAATTATTATAAAGAAATGAGCAGAATGAGCAGAATCTGATGCAAAC

QY 661 CTTCACCTGTTTCACCAACTGACTTATGCTTCACTGAACTATGTTAATCTGATGCAAAC

Db 662 CTTCACCTGTTTCACCAACTGACTTATGCTTCACTGAACTATGTTAATCTGATGCAAAC

QY 721 ACTTGGGTGCTTACACTGACTTATGCTTCACTGAACTGTTAATGTTAATCTGATGCAAAC

Db 722 ACTTGGGTGCTTACACTGACTTATGCTTCACTGAACTGTTAATGTTAATCTGATGCAAAC

QY 781 ATTAAATTATGAGAACTTACACAGAGGTCACACTACTGAACTTACAGTTAATCTGATGCAAAC

Db 782 ATTAAATTATGAGAACTTACACAGAGGTCACACTACTGAACTTACAGTTAATCTGATGCAAAC

QY 841 ATAGAAACGACTTGAAGATGCCCTGAGAGTCTCACTACTGAACTTACAGTTAATCTGATGCAAAC

Db 842 ATAGAAACGACTTGAAGATGCCCTGAGAGTCTCACTACTGAACTTACAGTTAATCTGATGCAAAC

QY 901 GAATATCTTATGAGAACTTACACAGAGGTCACACTACTGAACTTACAGTTAATCTGATGCAAAC

Db 902 GAATATCTTATGAGAACTTACACAGAGGTCACACTACTGAACTTACAGTTAATCTGATGCAAAC

QY 961 TATTCTAAAGACGATTTGAGAACTGAACTACATATCAGAACCAAGTTCTG 1020

Db 962 TATTCTAAAGACGATTTGAGAACTGAACTACATATCAGAACCAAGTTCTG 1021

QY 1021 TTTCACAGACGACTTGTACACCGTGTTCAGATCACATATGTTAACCT 1080

Db 1022 TTTCACAGACGACTTGTACACCGTGTTCAGATCACATATGTTAACCT 1081

QY 1081 TCAGATACACCTTATACACACTGCTGCTCTCATGACCCAGCACATCAAGTTTG 1140

Db 1082 TCAGATACACCTTATACACACTGCTGCTCTCATGACCCAGCACATCAAGTTTG 1141

QY 1141 ACTTACCGAAGCTTACAGATGATGTTGAAATGAGTAAAGCTTCAAGTAGGTC 1200

Db 1142 ACTTACCGAAGCTTACAGATGATGTTGAAATGAGTAAAGCTTCAAGTAGGTC 1201

QY 1201 TTGGAGACACTATCTACAAAAATGGATTAAAGACCTTCAGTC 1260

Db 1202 TTGGAGACACTATCTACAAAGATGTTGAAATGAGCTTCAAGTAGGTC 1261

QY 1261 ACGAGGAGATGCTCTTGAAATCTGGATTAGTGTCTGAAATCTGGATTAGTGTCTG 1320

Db 1262 ACGAGGAGATGCTCTTGAAATCTGGATTAGTGTCTG 1321

QY 1321 AGACATAAGAAACTGCACTGGTTGAGATACTGGTTAATTTGCTCAAT 1380

Db 1322 AGACATAAGAAACTGCACTGGTTGAGATACTGGTTAATTTGCTCAAT 1381

QY 1381 ATGCTTACTGACTCTGTTAGTGTACTGGTTGAGATACTGGTTAATTTGCTCA 1440

Db 1382 ATGCTTACTGACTCTGTTAGTGTACTGGTTGAGATACTGGTTAATTTGCTCA 1441

QY 1441 AGCATAAAATTAAGAGGCTTCAACAGCTGTTGAGCTTCAAGACTC 1500

Db 1442 AGCATAAAATTAAGAGGCTTCAACAGCTGTTGAGCTTCAAGACTC 1501

QY 1501 ATGTTGCTTCACTTAACTGACTGACCTTCTGGATGCTGAGCTTCAAGACTC 1560

Db 1502 ATGTTGCTTCACTTAACTGACTGACCTTCTGGATGCTGAGCTTCAAGACTC 1561

QY 1561 GTATGATCATGTTCACTTAACTGACTGACCTTCTGGATGCTGAGCTTCAAGACTC 1620

Db 1562 GTATGATCATGTTCACTTAACTGACTGACCTTCTGGATGCTGAGCTTCAAGACTC 1621

QY 1621 CAGAAGATGAGGCTTCAAAAGCAGGGACATCCATGATGTTGAGCTTCAAGACTC 1680

Db 1622 CAGAAGATGAGGCTTCAAAAGCAGGGACATCCATGATGTTGAGCTTCAAGACTC 1681

QY 1681 GAATTCGAAATATAGACGACTGAGTGTAGCTGAGCTTCAAGACTC 1740

US-09-949-002-65
; Sequence 65, Application US/09949002
; Patient No. 690016
; GENERAL INFORMATION:
Db 1742 TATAAGTGTGACTACCCGAAAGTTATAGAGGAAGGCCACTAAGGCTTCAGCTC 1801 ; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
Qy 1801 GAAATTATCTGCACATAACTCTGCTGATGTCACCATGTCACATGCTG 1800 ; TITLE OF INVENTION: AND USES THEREOF
Db 1802 GAATTATCTGCACATAACTCTGCTGATGTCACCATGTCACATGCTG 1861 ; APPLICANT: VENTER, J. Craig et al.
Qy 1861 GCTGTGACTGTGACTCCCTCTGCATCTACTTGATCTGCTGGTATCTCGGATGGT 1920 ; CURRENT APPLICATION NUMBER: US/09/949, 002
Db 1862 GTGTGACTGTGACTCCCTCTGCATCTACTTGATCTGCTGGTATCTCGGATGGT 1920 ; CURRENT FILING DATE: 2000-01-28
Qy 1921 TGCCTAGTGGACCCAGACTCGGCCAGGGCCAGAACATACCCCTAGAGAACCTCCAAAGA 1980 ; PRIORITY NUMBER: 60/231, 401
Db 1922 TGCCTAGTGGACCCAGACTCGGCCAGGGCCAGAACATACCCCTAGAGAACCTCCAAAGA 1981 ; SOFTWARE: FastSEQ for Windows Version 4.0
Qy 1981 AACCTCGAGTTCATGCTTTATTCTCATAGACATGATCTGCTGGTGAAGT 2040 ; NUMBER OF SEQ ID NOS: 10823
Db 1982 AACCTCGAGTTCATGCTTTATTCTCATAGACATGATCTGCTGGTGAAGT 2041 ; LENGTH: 2366
Qy 2041 GRATGSGTACTCTACCTAGAAAGAGATACAGATTCTTCAAGGAACCTT 2100 ; SEQ ID NO: 65
Db 2042 GATTTGGTACTCTACCTAGAAAGAGATACAGATTCTTCAAGGAACCTT 2101 ; ORGANISM: Human
Qy 2101 GTCCTCGGCAAGACATGTGGAATATCTCACTGCTGAGAGAGTACAATCC 2160 ; TYPE: DNA
Db 2102 GTCCTCGGCAAGACATGTGGAATATCTCACTGCTGAGAGAGTACAATCC 2161 ; LENGTH: 2366
Qy 2161 ATCTTGTGTTCTCCAACTTGTGCAAGTGTGAGGGTGCATTAATTT 2220 ; US-09-949-002-65
Db 2162 ATCTTGTGTTCTCCAACTTGTGCAAGTGTGAGGGTGCATTAATTT 2221 ;
Qy 2221 GCCCATCACAACTCTCTCATGAGAGCTTAACTTAACCTCACTCTGTGACC 2280 ;
Db 2222 GCCCATCACAACTCTCTCATGAGAGCTTAACTTAACCTCACTCTGTGACC 2281 ;
Qy 2281 ATTCCACAGAGACGATTCACACAGTACAGTACAGTACACAGCTGAGGGCTCATGACCGAGCG 2340 ;
Db 2282 ATTCCACAGAGACGATTCACACAGTACAGTACAGTACACAGCTGAGGGCTCATGACCGAGCG 2341 ;
Qy 2341 ACTTATTGCACTGGCCAAAGGAAAAGCAACGTTGGCTCTTGGCTACATTAGA 2400 ;
Db 2342 ACTTATTGCACTGGCCAAAGGAAAAGCAACGTTGGCTCTTGGCTACATTAGA 2401 ;
Qy 2401 GCGCCTTTATATGAATTACACTGTCTGAAACAACTGATGTTGAATCTTTAAA 2460 ;
Db 2402 GCGCCTTTATATGAATTACACTGTCTGAAACAACTGATGTTGAATCTTTAAA 2461 ;
Qy 2461 ATTGGAATTCACTTAGAACATTAATTACTTGATGATGTTGAATCTTTAAA 2520 ;
Db 2462 ATTGGAATTCACTTAGAACATTAATTACTTGATGATGTTGAATCTTTAAA 2521 ;
Qy 2521 GTAAAGTAACTCTGGGGACTGAGCTCATTATCTCATGCTTCAGGAAGACTAAC 2580 ;
Db 2522 GTAAAGTAACTCTGGGGACTGAGCTCATTATCTCATGCTTCAGGAAGACTAAC 2581 ;
Qy 2581 AACAAATGTTCATCTGGGGACTGAGCTCAGGCTGAGGTTAGCTGCGCTTAGAGAC 2640 ;
Db 2582 AACAAATGTTCATCTGGGGACTGAGCTCAGGCTGAGGTTAGCTGCGCTTAGAGAC 2641 ;
Qy 2641 AGCCCCAGTCCTCTGGGGACTGAGCTCAGGCTGAGGTTAGCTGCGCTTAGAGAC 2700 ;
Db 2642 AGCCCCAGTCCTCTGGGGACTGAGCTCAGGCTGAGGTTAGCTGCGCTTAGAGAC 2701 ;
Qy 2701 ATGCTCAGTTTCAGTCCCTCACTCTCTTCCAATGGATTCTGTG 2753 ;
Db 2702 ATGCTCAGTTTCAGTCCCTCACTCTCTTCCAATGGATTCTGTG 2754 ;

QY 802 ACCAGAGGTCAACCTTACTGAAATTACCCCAACACATAGAACGACTGGAAATGC 861
 Db 721 CAAACAAATCCAAAGTTTACCTTCAGCTTAACTTAACAACTGAACTGGAACT 780
 QY 862 CTGGTCAGAGTCTTCATTTCTTGCCCCAACCTGTGGATACTCAATATTAAAT 921
 Db 781 TTCATTPAGGATCTCCAGCTGGTTGGCATACACTGTATGTTCTCAATTCAAC 840
 QY 922 TTAACATAATGAAAGCATTCAGTGTGAGAACATTACTTATCTAAACACATGAA 981
 Db 841 GTGAAGCTACKGGTAGCTGACTTCAGACATTGATTCGGACTCTTCAG 900
 QY 982 CCATTCACAATAGAACATACGACACCAGTTTCTGTTACAGACAGCTTGAC 1041
 Db 901 GCCTTGCTATACACCGATGTTCTAGCGATTTGTTCCGAACTTATCAT 960
 QY 1042 ACCGGTGTTCCTGAGATGAAATTATGATGTTAACATTGATGTTACCTTACAC 1101
 Db 961 GAAATCTTTCGAATGAACTAAATTCACAGTGTGTTGGACAGATGGCCAC 1020
 QY 1102 ATGCCTGTCCTCATGACCAGCACATTCACTTGTGACTTTACCCACAGTTTC 1161
 Db 1021 ATGCCTGCCCACATCCCAAATTAGGCCCTTCTGCAATTCCAAATCTCTA 1080
 QY 1162 ACAGATAGTATTGAAATGTTCCACGTTACGTTAATTGGAGAACCTTACAC 1221
 Db 1081 ACAGACAGGTTTGTGAAATTGTTGGCACCTACTGAGTGGAGACATTATCAA 1140
 QY 1222 AAAATGGATTAAAGACCTTCAAGTAGTCTCATGAGGAAGGATACCTTCTTG 1281
 Db 1141 ATGAACTAAATTAAAGACTTCAAAATACGTTCAATATGACTACAGTGTCTG 1200
 QY 1282 GAAATCTGTTGTGACTGGAATTTGGATCTGACATATAAGAAACTGCACT 1341
 Db 1201 GAAACATTGGATATTGACGAGATTCTGTAAGCTATGATGAAAGAAGGAGCT 1260
 QY 1342 TGGITGTGAGGATAGCTGCTTAATTGCTCAATATGCTCTGACTCTGTT 1401
 Db 1261 TGGACTAAAGTTTAAAGTTAAATGTTCAATATGACTACTGACTATTTC 1320
 QY 1402 AGATGTTTACCTCCAGGATTAAGGACTTCTTCAGAGATAATAAGGGTT 1461
 Db 1321 AGATGTTTACCTCCAGGATTAAGGACTTCTTCAGAGATAATAAGGGTT 1380
 QY 1462 CCTAAACAACTGTAAACTCTGAAAGTTTGTGAGAACACTAACTGTTCTTAAATT 1521
 Db 1381 OCTAAACAAAGTGTAAACTCTGAAAGCTTGTGAGAACACTAACTGTTCTTAAATT 1440
 QY 1522 ACTGACCTCTGGATGTGGAGCTTAGCGCCTTCTGTTGATGATCATGATCAAT 1581
 Db 1441 ACTGACCTCTGGATGTGGAGCTTAGCGCCTTCTGTTGATGATCATGATCAAT 1500
 QY 1582 TAGTTCCACCCATGGCTGATTCTCAGAGCTGCCAGAGTGAGGCTAA 1641
 Db 1501 TCAGTTCCACCCATGGCTGATTCTCAGAGCTGCCAGAGTGAGGCTAA 1560
 QY 1642 CGAGGGGACAACTCCATCCAACTGACTCTGAGGATTCGAAATAATAGAC 1701
 Db 1561 CGAGGGGACAACTCCATCCAACTGACTCTGAGGATTCGAAATAATAGAC 1620
 QY 1702 CAAGATCACTGAACTGTTAGGGCTGGCTGATCTTAACTGTTACCTGAGAA 1761
 Db 1621 CAAGATCACTGAACTGTTAGGGCTGGCTGATCTTAACTGTTACCTGAGAA 1680
 QY 1762 AGTTATGAGGAGGCCACTAAAGGACTTACATGCTGAAATTCTGAACTAACT 1821
 Db 1681 AGTTATGAGGAGGCCACTAAAGGACTTACATGCTGAAATTCTGAACTAACT 1740
 QY 1822 CTGCTGATCGTACCATGAGGCTGGCTGAGCTGACTGTTACCTGCTC 1881
 Db 1741 CTGCTGATCGTACCATGAGGCTGGCTGAGCTGACTGTTACCTGCTC 1800
 QY 1882 TGCATCTACTTGGATCTGCCCTGGTAACTCAGGATGGCTGCCAGGACCTGG 1941

RESULT 6
 US-09-949-002-236
 Sequence 236 Application US/09949002
 ; Patent No. 6300016
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: CL000790
 ; CURRENT APPLICATION NUMBER: US/09/949, 002
 ; PRIORITY APPLICATION NUMBER: 6/0/231, 401
 ; PRIORITY FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 10823
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 236
 ; LENGTH: 2367
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(2367)
 ; OTHER INFORMATION: n = A, T, C or G
 ; US-09-949-002-236
 Query Match 51.8%; Score 14264; DB 3; Length 2367;
 Best Local Similarity 76.1%; Pred. No. 0;
 Matches 1785; Conservative 0; Mismatches 552; Indels 8; Gaps 2;
 QY 88 ATGTTAAAGCTTCATTGTTGGCTATGATCATAATTAGTGGACCAAGTCAG 147
 Db 1 ATGACTGACATCTCCATTGCCCCATTATCTCATGTTAACTTCAGATCAGAAATCAA 60

QY	148	TTCCTCCGACGGAAATGATTGCACTAGAGACAACTGCAAAAGGGCTTATTCATGTTCA	207	QY	1220	AAAAATGGATAAAGACCTTCAAGTAGGTCTCATGAGAAGATAGCCTCT	1279
Db	61	TTATCTGAGAGAAGTGTGATTGTTAGTGTGATAGTCATAAACAGGTCTCACACGTTCT	120	Db	1141	AATGATCAATAAAGACCTTCAAAATAGTGAAATGACTACAGATGAGCTC	1200
QY	208	AAAGACCTTACCGTGAAACCAAAGCTTAAATGTTGCTCAGAACCTGTCAGACTGACTT	267	QY	1280	TGGAATTAATCTGATGTTAGTGTGAAATCTTGGAACTTGGAATCTGGAGACATAAAGAACTGCA	1339
Db	121	AAAGACCTTACCGTGAAACCAAAGCTTAAATGTTGCTCAGAACCTGTCAGACTGACTT	267	Db	1201	TGCAACATGATATTAGCCGAACTCTGTAAGCTGAAATGAGCTACAGATGAGCTC	1260
QY	268	CAGGTCTCTGACATGAGGTTCTATCGAGGTTGACAGTTTGAGACTTCCCATACAGA	327	QY	1340	CTGGGTGAGGTGTTGTTAAATTGTCATAATGCTACTGACTCTGTT	1399
Db	181	TGAGCTTCTGACATCTATCGTCAAACTGCAAACTGAGATTGATATTCTGATATAGA	240	Db	1261	CTGGACTAAAGTTTAACTTAAATATCTCAATAATGACTGACATT	1320
QY	328	ATCCAGCTACTTGATTAGTGTTCAGGTTCAAGGTTCAACGGATTAGATTTGGATTA	387	QY	1400	TCAGATGTTACTCTCCAGGATCAAGGACTGTTAGATTTGGATTA	1459
Db	241	ATCCAGTATCTGATATCGTGTCAATTACCGGAAATGTTGAGATCTGACATGTTG	300	Db	1321	TCGATGTTACTCCAGGATCAAGTGTACTGATCTCACNGATAATAAGGCA	1380
QY	388	TCTCATATACTGCAAGAATATCTGCCATCC - TATTGAGTTTCGGATTAG	445	QY	1460	TTCCTAAACAAGCTGAAACTGCAAGACTGTTGCAAGAACTCATGTTGCTTCATTT	1519
Db	301	TCCACAHANAGHTGGTGAAGATTCTGACCCCTACTGGAACCTCAGACTG	360	Db	1381	TICCTAAACAAGCTGAAACTGCAAGACTGTTGCAAGAACTCATGTT	1440
QY	446	ATCTCTCATCTAATGATTCAAGCCCTGCCCATGTAAGGATTGGCAACTTAC	505	QY	1520	TAATGCCTCTGGTGTGCGCTTACAGCTTCTGTTATGATCATGATGACA	1579
Db	361	ACCTGTCATTATGATTCATGTTATGCTGCTGCTATGCAAGAAGTGTGGCATATGTC	420	Db	1441	TAATGACTCTCTGGATGTCAGCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCT	1500
QY	506	AACTGAATTCTGGATTGAGTGTGCTATGAACTGCAAATTTAGATTTGGCTTAC	565	QY	1580	ATCAGTTCCACCCATCCTGGTGTGCGCTTACAGCTTCTGAGCTGCGCAATG	1639
Db	421	AACTAAATTCCTGGGTGAGCACCACACTTAGAAATACTAGTGTGTCGCAAT	480	Db	1501	ATCAGTTCCACCCATCCTGGTGTGCGCTTACAGCTTCTGAGCTTCTGAGCT	1560
QY	566	CTCACTTGACTCTAAGTTATCTCTGGTTAGAAATTATATAAGAAATG	625	QY	1640	AAGCAGGGACATCCATCTCCATGTTGACTCTGAGCTTGTCAAATTTAG	1699
Db	481	CCTCATTTGAAATCTAGCAAGCTTCTGCTGTTAGGAGACTTATGGGAAAGAAG	540	Db	1561	ANGCAGGGACATCTCTGAGCTGAGCTTGTCAAATTTAG	1620
QY	626	AGACAGAAAGCTACAAATCTGATGAAACCCCTCACCTGTTAACCAACTA	685	QY	1700	ACCAACTTCACTGAGTGTAGGGCTTACAGCTTCTGCTTATAGTGTACTACCC	1759
Db	541	ACCTTGAGGGCTTCAGACTTAACCTGAGTGTGAGCTGTCACATGTCACAA	600	Db	1681	AAAGTTATAGGAAACCTCTAATGAGCTTCTGAGCTTCTGAGCTTCTGAGCT	1680
QY	686	GTTTATGCTTCCAAAGTGTGACATATCTGTTAACTTTGGTGTGAGCTGAA	745	QY	1820	CTCTGCTGATGTTGCTCACCATCTGGCCACCATGCTGTTGGCTGTGACTTGACCTCC	1879
Db	601	AGAAATTCATTTATTGAGTGTGAGCTGAACTGTCACATGTCACATCTA	660	Db	1741	CTCTGCTGATGTCACCATCTGGCTGAGCTTCTGAGCTTCTGAGCT	1800
QY	746	ATTTAAAT----TGAATATGAACTCTCAAGTTTAAATTATGACAC	799	QY	1880	TCTGCATCTACTGAGTGTGCTGCTGTTGCTGTTGCTGAGCTTCTGAGCT	1939
Db	661	ATATCAAATGTTGCTAGAAATACTGTTCTTACTCTGTTGCTGAAAC	720	Db	1801	TCTGAGCTACTGAGTGTGCTGCTGCTGAGCTTCTGAGCTTCTGAGCT	1860
QY	800	TCACCAAGGGTCACCTTATGAAATTCTCTCAACCAATGAGACTGGAAAT	859	QY	1940	GGCGAGGGCCAGGAACATACCTGCTGAGACTCTGAAAGAACCTCCAGTTCTGAGCT	1999
Db	721	TTCACAACTAACCAAACTTACAAATTCTACAAATGAACTGAACTGAAAT	780	Db	1861	GGCGAGGGCCAGGAACATACCTGAGAGACTCTGAAAGAACCTCCAGTTCTGAGCT	1920
QY	860	GCCTGGTCAGAGTCTTCAATTCTGAGGTTGGCTGAGCTGAA	919	QY	2000	TATTCATATGAGACATGTTCTGCTGGTGAAGAAGTGTACTTACTG	2059
Db	781	CTTCACTTCTCCAGTCTCAGTGTGTTGGCTACAACTGTTCTCAATTCAA	840	Db	1921	TATTCATATGAGGCTGAGCTTCTGGTGAAGAAGTGTACTTACTG	1980
QY	920	ATTAACAATATTGAAAGCATCTGAGAGATTCTTACTTACCTAACGACATG	979	QY	2060	AAAAAGGAGATACTGAGTGTGCTCTGAGGAGACTTGTGCTGGAGACATTG	2119
Db	841	ACGTGAGACTACGGTCAGCTGAGCTTCTGGTGAAGAAGTGTACTTACTG	900	Db	1981	AGAAAGGAGATGAGCTGAGTGTGCTGAGAGACTTACGTCATGAGACATTG	2040
QY	980	AAGCATGACATAGACATATCACGACCAAGTTCTCTTACAGACAGCTGT	1039	Db	2120	TGGAATATCATCAACTGCTGAGAGACTTACGTCATGAGACATTGCTCT	2179
Db	901	AGGCCTTGTCTCATCCAACTGAGCTTCTGGTGAAGAAGTGTACTTACTG	960	Db	2041	TGGAATATCATCACTGAGAGACTTACGTCATGAGACATTGCTCT	2100
QY	1040	ACACCGGTTCTGAGATGACATTGTTAACATTCTGAGTACACTTTATAC	1099	QY	2180	ACTTGTCCAGTGTGAGTGTGCTGAGACTTATGCCCACACATCTCTC	2239
Db	961	ATGAATCTTCTGAAATGACATCAACATTCTGAGTACACTGAGCTGTC	1020	Db	2101	ACTTGTCCAGTGTGAGTGTGCTGAGACTTATGCCCACACATCTCTC	2160
QY	1100	ACATGCTGTCCTCATGACACATCAAGTTTGTACTTACCTACAGCTT	1159	QY	2240	ATGAGGATCTAATCTGCTGAGGCTCTCATGACAGCAGCTTC	2299
Db	1021	ACATGCTTGCCTCATCAAATTAGCCGTTCTGAGTATTTCCATATCT	1080	Db	2161	ATGAAGGATCTAATCTGCTGAGGCTCTCATGACAGCAGCTTC	2220
QY	1160	TCTCAGATAGATTGAAATGTCAGGTTAGTAAATTGGAGACACTTACCTAC	1219	QY	2300	CCAACAGTACACAGCTGAGGCTCTCATGACCCGCGACTTATTCAGTGGCCA	2359

RESULT 7

US-09-949-002-637
; Sequence 637, Application US/09949002
; Patent No. 6300016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: WITHIN INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949, 002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 637
; LENGTH: 6392

TYPE: DNA
ORGANISM: Human
FEATURE:
LOCATION: misc_feature
(1) : (6392)
OTHER INFORMATION: n = A,T,C or G

US-09-949-002-637

Query Match 50.6%; Score 1392; DB 3; Length 6392;
Best Local Similarity 75.3%; Pred. No. 0; Mismatches 552; Indels 33; Gaps 3;
Matches 1785; Conservative 0; MisMatches 552; Indels 33; Gaps 3;

QY 88 ATGTTAAACGCTCCATTGTCCTTATGATCATTAATAGTTGAACTGGACCGAATTCAG 147
Db 2001 ATGACTTACGATCTCCATTGTCCTTATCAGTTGAACTGGACCGAATTCAG 2060

QY 148 TCTCCGACGGAATAGTTCAGTAGACAGTCAAAAGAGCTTATTCAGATGTCCA 207
Db 2061 TTATCGAAGAAAGTGTAGTTGATAAGTCAAAAGGTCTCATCACGTCT 2120

QY 208 AAAGACCTACGCTGAAACCAAGCTTAACTATGCTCAGACTACATGCTGAGCT 267
Db 2121 AAAGACCTATCCAGAACACAATCTAAATATGCAAAATTCAGCT 2180

QY 268 CAGGTCCTGACATGAGCTTCTATCAGAGTTGACAGTTGAGCTTCCATACAGA 327
Db 2181 TGGACTCTGACATCTTACGTGCAAACTGAGATTGATAATTCATATAAGA 2240

QY 328 ATCCACSTACTGTATTAAAGTTCAAGTCACAGGTTAGATATTTGGATTA 387
Db 2241 ATCCAGPACTTGTGATACTAGTGTTCAAATCAACAGGATGGATACTTGGATTG 2300

QY 388 TCTCATATACT-----AGTTGAAAGATACTCTGCATCC 422
Db 2301 TCCCAACANNNNNNNNNNNNNNNNNCAACACAGTTGAGATTCCTGCACCC 2360

QY 423 --TATGTCGAACTTCAGGCAATTAGTCTCTCATTCATGTTCTGGCCCTGCACCC 480
Db 2361 CTACTGTGAACTCTGACATGCTGACCTTGATGCTGCTGCATA 2420

QY 481 TGTGAGGAATGTCGACACTTACACTGATTCTGCGATTGAGCTG 540
Db 2421 TGCAGAAGAGTTTGGCAATATGCTCAACTAAATTCTGGGTGAGCACCACACTA 2480

QY 541 CAAATATGATTGCTGCCATTGCTCACTGCTACTTGTCAATTCTCTGGATT 600
Db 2481 GAAATCTAGTGTCTGCCTATGCTATGAAATTCAGCAAGCTCTRGCTGTTA 2540

QY 601 AGAAATTATATAAAGAAAATGAGGAGCAGAAGTCTACAATCTGAATGCAA 660
Db 2541 GGAGAGCTATGGGAAAGAGACCTGGCTTGAGATTAACACTGAAGT 2600

QY 661 CTTCACCTTTCACCCACACTAGTTATCGTATCCAGTAACTTACACTTAAT 720
Db 2601 CTGCACTTGTGTCACACAGTCTTCAAGTACACTGAGCT 2660

QY 721 ACTTGGGCTTACACTGACTATTAAT----TGAATGAGACAACTGCTAA 774
Db 2661 ACTGTAGCAAATCTGGAACTATCTAAATCATCAATGTTGCTGAGATAACATGTCT 2720

QY 775 GTTCTATAAATTATCAGAACTCCACAGAGGTTCAACTTACTGAATTACCTC 834
Db 2721 TACTCTAGTATCTGGCAACTTACACAACTTCAAGTATCAATCTTACCTA 2780

QY 835 AACACATAGAAACGACTTGAATGCTGTCAGTCTTCATTAATCTGGCAA 894
Db 2781 AACACATGAAACACTGGATCTTCTTATTAGATCCACAGCTGCT 2840

QY 895 CCTGTGCAATCTCAATTACATTAACATTAATGAAAGCATCTGAGAAGAT 954
Db 2841 ACTGTATGGTATTCTCAATTCAACAGTGTGAGCTACAGGTCTGAGAT 2900

QY 955 TTACTATTCTAAAGACGTTGTTACCCGTTCTGAGTAACTTACAGATA 1014
Db 2901 TTGATGATTCGCAACTTCTGAGTAACTTACAGATACTTACACAGTGT 2960

QY 1015 TTCTCTTTACAGACGTTGTTACCCGTTCTGAGTAACTTACAGATA 1074
Db 2961 TTGGTTTCGCAAGTTATCTATGAAATCTTCTGAGTAACTTACAGATA 3020

QY 1075 ACCATTGAGATACCTTATACACACTCTGTCCTGACCCACATCAAG 1134
Db 3021 ACAGTGTCTGGTACACGATCTGTCATGCTTGCCTCATCAAATTAGCCGCTCTG 3080

QY 1135 TTGAGACTTACCCAGAAAGCTTCACTGAGATAGTTTGAATAAGACCTTCCACGTIA 1194
Db 3081 CATTGGATTTCACATATCTCTTACAGACAGGTTTGTGAAATTGGCACCT 3140

QY 1195 GTTAATGGAGACACTTACCTACAAAAATGGATAAAAGACCTTCAAGTAGGT 1254
Db 3141 ACTGAGTTGGAGACACTTACCTACAGATGATCATTAAGAACCTTCAGAATAGCT 3200

QY 1255 CTCATGAGGAGATGCTCTTGTGAAATCTGGATTCTGGAATTCTTGAA 1314
Db 3201 GAAATGACTACAGAGTAACTGCTCTGCAACATTTGGATAATTAGCCGATCTGAGC 3260

QY 1315 TCTGGAGACTTACAAAGAAACTGCTCTGGTTGAGAGTTAGTGTAAATTGCT 1374
Db 3261 TATGTCGAAAGAAGGAGACTGTTCTGAGTAACTTAAATGTT 3320

QY 1375 TCAATATGCTACTGACTCTGTTGAGTTGAGCTTACCTCCAGGATCAAGGACTGT 1434
Db 3321 TCAATATGCTACTGACTCTGTTGAGTTGAGCTTACCTCCAGGATCAAGGACTGT 3380

QY 1435 CTTCACGCTAAATAAAGACGCTTCAACAGCTTAAACTGAGCTTGTGAA 1494
Db 3381 CTTCACGCTAAATAAAGACGCTTCAACAGCTTGTGAA 3440

QY 1495 GAACCTGAGTTGCTTCACTTCACTGACTCTGGAGCTTCTGGAGCTTGGAGC 1554
Db 3441 GAACCTGAGTTGCTTCACTTCACTGACTCTGGAGCTTCTGGAGC 3500

QY 1555 CTTCACGCTTGTGCTTCACTTCACTGACTCTGGAGCTTCTGGAGC 1614
Db 3501 CTTCACGCTTGTGCTTCACTTCACTGACTCTGGAGCTTCTGGAGC 3560

Qy 1615 ACCTGGCAGAGATGAGTCATAAAGCAAGGACATCCATTCCATGACCTTGAG ; SEQ ID NO: 808
Db 3561 AGCTGCCAGAGATGAGTCATAAAGCAAGGACATCCATTCCATGACCTTGAG ; LENGTH: 6392
Qy 1675 CTAAGAGATTGTCATAAAATAAGACAGATGAGTGTAGAGGGCTGCCT 1734 ; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6392)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-002-808

Query Match 50.6%; Score 1392; DB 3; Length 6392;
Best Local Similarity 75.3%; Pred. No. 0; Mismatches 552; Indels 33; Gaps 3;
Matches 1785; Conservative 0;

Qy 3741 ATGCTGTTGATATCTGCAACATAACTCTGCTGATCTGCACATCGTCCATGAGCTG 3800 ;
Db 1855 GTGTTGGCTGACTGTGACCTGGACCTCCCTGCACTACTGTGACTGCTGCTGTG 3740 ;
Qy 1795 ATGCTGTTGATATCTGCAACATAACTCTGCTGATCTGCACATCGTCCATGAGCTG 1854 ;
Db 3801 GTGTTGGCTGACTGTGACCTGGACCTCCCTGCACTACTGTGACTGCTGCTGTG 3860 ;
Qy 1915 ATGCTGTTGACCTGGCAAGCTCGCCAGGAGCTGCTGATCTGCACATCGTCCATGAGCTG 3800 ;
Db 3861 ATGCTGTTGACCTGGCAAGCTGGCCAGGAGCTGCTGATCTGCACATCGTCCATGAGCTG 1914 ;
Qy 3921 CAAGAACCTCCAGTTCTGCACTTTATGTCAGATGTTCTGAGAAAGAGACTC 1974 ;
Db 3881 AAAGTGTGATGTTGCTACCTTAGAAAAGAGATACTACAGATTGTCATGAGG 2094 ;
Qy 3980 CAAGAACCTCCAGTTCTGCACTTTATGTCAGATGTTCTGAGAAAGAGACTC 3920 ;
Db 3981 AAAGAAGATTTGTCAGCTTCACTAGAGAAAGAGATGAGTGTGAGCTTCTGAGA 4040 ;
Qy 2095 ACTTGTGTCCTGCAAGAGCTGTTGAAATATCATCAACTGTTCTGAGAGTAC 2154 ;
Db 4041 ACTTGTGTCCTGCAAGAGCTGTTGAAATATCATCACTGTTCTGAGAGTAC 4100 ;
Db 2155 AAGTCCTCTTGTCTCCAACTTGTCAAGGTGTTGCAAGGCTTCTGAGACT 2214 ;
Db 4101 AAGTCCTCTTGTCTCCAACTTGTCAAGGTGTTGCAAGGCTTCTGAGACT 4160 ;
Qy 2215 TATTGCGCCATCACAACTCTCTCATGAAAGATCTAACTTAATCTATCTACTG 2274 ;
Db 4161 TACTTGCCTCACATCTCTCATGAAAGATCTAACTTAATCTATCTACTG 4220 ;
Db 2275 GRACCCATTCAGCAAGACAGATCCAAACAGTACCAAGCTGAGGCTCTGAGCG 2334 ;
Db 4221 GRACCCATTCAGCAAGACAGATCCAAACAGTACCAAGCTGAGGCTCTGAGCG 4280 ;
Qy 2335 CRGGGACTTATTGCACTGCCAAGGAAAGCAACCTGGCTCTTGGCTAC 2394 ;
Db 4281 AGGAGCACTTATGGATGCCAAGGAAGAGCAACGGGCCCTTGGCTAC 4340 ;
Qy 2395 ATTAGAGCCGCTTTAATGAAATTACA 2424 ;
Db 4341 TTAAGGCAGCCATTAAATTAGCTGACA 4370 ;

RESULT 8
US-09-949-002-B08
; Sequence 808, Application US/09919002
; Patient No. 630016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949, 002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231, 401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSEQ for Windows version 4.0


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; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 28.2%; Score 777.2; DB 3; Length 3462;
Best Local Similarity 59.8%; Pred. No. 3e-209; Mismatches 948; Indels 30; Gaps 8;
Matches 1456; Conservative 0; Misnmatches 948; Indels 30; Gaps 8;

QY 45 TTGAGTAGCCACTGCACATCATGACCAAGAACACTATGTTAAAGCTTCCA 104
Db 77 TCGAGGAATAAGTGTAAATCTTGGAAATACATGAGACTCATGAGAACATTACAT 136
QY 105 TTGTTGTCCTTATGATCATATAAGTGTGGACCAGATCCAGTTCGGGAAATGA 164
Db 197 ACTGATGCCAACATGCCAACATGTCCTAGAAAGGTTCGGCAGACTGACCCAGC 256
Db 137 ATTGCTGATGTTGTTGATGAGACAGCAGGAGGTGATGTCAGAGTGTGAG 196
QY 165 ATTGCGAGTAGACAAGTCAGAACAGAGCTTATCATGTCAGAACAGCTTACCGGTGAA 224
Db 225 ACCAAAGTCTAGATGTTGAGACTAATGCCAGAGTTCAGTCTAGTGTGAG 284
Db 257 CACAAAGCACAGTGGATTATCTATAACCTCTTTCAACTCCAGAGTTGATTTCA 316
Qy 285 CCTCTPATCAGTTGAGCTTGACTTCCATAACGAAATCCGACTACTGATT 344
Db 317 TCTGTCGCCAACATGAGTTGAGCTTGACTTCCATACAGAACATCACAGTC 376
QY 345 AAGTGTTCAGTCACCGGATTAGATAATTGGATTATCTCATATCAGTGTCA 404
Db 377 CAAAACCTTGAATTCAAAGAGTTAGATATTAGATTTGTCATAACAGACTGAA 436
QY 405 AAAGATATCCTCCATCTATGTCAGTTGAGCTTCCGGATTAACTCTCATGATT 464
Db 437 GAGTGTRACTGGTATTACTGGAGCTCTAGGTTAGACTTACACTGATTCTGGATT 496
Qy 465 CAAGGCCCTGCCATCTGTAAGAAATTGGCAACTTACACTGATTCTGGATT 524
Db 497 TACACCATGCCPATCTGTGAGCAAGCTGGCACATGTCACCTGGAAATCTAGTT 556
QY 525 GAGTGTCTATGAACTGCAAATTAGATTGCTGCCATTGTCACGTGCTAAGTAA 584
Db 557 GAGTGTGCGAAATACTAAATCAGATTCCAGAAATTGTCATCTGCACTAAATAC 616
QY 585 TATCCTCTGATTAAAGAAATTATAAAAGAAATGAGACAGAAATCTACAAAT 644
Db 617 TGTCTCTTAGGATTGAGACTCTCT----CATTATGAGAGGTGACCTGCCAT 670
Qy 645 TCTGAGTGCAGAACACCCTCACTTGTGTTTCACTGACGAGGTTACCTCAAGT 704
Db 671 CTAAACACACAAACGCACTGCACTTGTGTTTCACTGACGAGGTTACCTCAAGT 730
QY 705 GACATATCAGTTAATCTTGGGCTTACAGACTAATTAATGATGATGAA 764
Db 731 CGGTGATGAGATCAAGCTTCAAAATATTAGAAATGACAATA-TGATGCAAAAGCC 789
QY 765 CTAAGTGTCAAGTTTCATTAATTTTCAAGACTCACCAAGGAGGTCAACCTACTGAA 824
Db 790 AATTGTTAGTTAGAATGCAAGAAATCTTGTAGAAATGCTAGAC-ATCGGT 847
Qy 825 TTTTACCTCACCACATAGAAAGACTGGAATGCTGTCAGAGGTTCACTTCT 884
Db 848 TCTATGCTTAATGAGTTGTTACTCTGGGAGGACCTTCTTCACTTCAATTGT 907

QY 885 TTGGCCAAACCTGGGAATATCATAATTAAATTAATTAATGAAAGCATRC 944
Db 908 TTGGCATACATCAGTGGAACTTCAGATCCGAAATGACTTTGTGTGTAAAGCTTA 967
QY 945 TGAAGAGA-----TTTACTTATCTAAACGACATGAAAGCATGCAATAGACA 998
Db 968 TCTTGACACAAATTGACTACTCAATACTGTAATGAGAACTTAAATGGAGCA 1027
QY 999 TATCAGAACAGTTCTGTGTTCCAGACAGCTTGTACCCGIGTTCTGAGAT 1058
Db 1028 TGTACATTCAGAGTTTACATTCACAGGATAAACTCTATTGCTTTGACAAAT 1087
Db 1059 GAACTTATGTTGTAACCTTTGAGTACACCTTTATCACAGNGCTGTCCTCAGC 1118
Db 1088 GGACATAGAAACCTGACAAATGCAATGCAACATGCTGCTTCCGAATTA 1147
QY 1119 ACCAAGCACATCAAGTTGACTTTGACTTACCGAGACGTTTCAGAGATTTGA 1178
Db 1148 TCCTACGAATTCGAAATTCAGTCAATTAAATTGCAATATTTGAAATTAACAGACAGTGTAA 1207
QY 1179 AAATGTTCCAGTGTAGTTAAATTGGAGACTTACCGAGACGTTTCAGAGATTTGA 1228
Db 1208 AGAACTATCCAACTCCACTGAACTCTCTGTTGATGGCAAAACTGGAGAC 1267
QY 1229 CCTTTTCAAGTAGTCATGACGAGAATGCTCTTGGAAATACTGGAGTTAG 1298
Db 1268 ACTTCTCTTACTAAGTTGCTTGTCTAACACAC--CCTTGGACACTTGGATCTGAG 1324
QY 1299 CTGGAATCTTGGATCTGAGCTGAGATAAGAAACTGCACTTGGTTGAGATPATG 1358
Db 1325 TCAAATCTTACAC--ATAAAATGTAAGAAATTGTCATGCGAGAACITGTGT 1381
QY 1359 GGTGTAATTGTCCTCAATATGCTACTGACTCTGTTTCAAGTTACCTCCAG 1418
Db 1382 CAATATGCACTGTCATACAAATATTGTCGTTGAGGTGCTGCCAAAG 1441
Db 1419 GATCAAGGTACTGTTTCAAGCAATAATAAGAGGTTCAAAAGTGTAA 1478
Db 1442 TATTCATACACTGACCTAAATAATRACCAATTCACATGACTTAAAGACTATCA 1501
QY 1479 ACTGGAGCTTGCAGAACCTCAAGTGTGCTTCAATCTTAACTGACCTTCCTGGATG 1538
Db 1502 TCTGATGCGCTTACAGAACTAAATGCAATTATGCAATTATTTCTAACTGATCTCCGGATG 1561
QY 1539 TEGCAGCTTGCAGCCCTCTGATATTGATCATGTCACAAATTCAGTTCCACCCATC 1598
Db 1562 CAGTCATTCTGAGACTTTCAGTCACTGAACTGAACTCATCTACCCATC 1621
Db 1599 GCTGAGTTCTCCAGCTGGCAGAGTCAATAAGAGGTTCAAACTCCATT 1658
Db 1622 TCTGGTTTGTCTGAGCTCCAGGAGTAACTCTAAATGGGGGAAGTCATT 1681
QY 1659 CCAATGACCTGTCAGCTGAGCTTGTCAAATATGACCAAGTCAAGTGAAGT 1718
Db 1682 CGGTGTTACCTGTAATA--AAATTCATCAGTCAAACTTCAATTCAGGTCAT 1738
QY 1719 GTTAGAGGGCTGCCATTCTATAGTGTGACTTACCCAGAAAGTTAGAGGAGCC 1778
Db 1739 GATGGTTGGAGTGTGAGCTCATCCTGAACTCCCTTAACTTAAGGGAACTAG 1798
QY 1779 ACTAAGGACTTCAATGTCAGAAATATCTGCAACATRACTCTGGTGTACCAT 1838
Db 1799 GTAAAGAGCTTCATCTCCAGAAATTCTGCAACACTCTGTGTGTCACCAT 1858
Qy 1839 CGGTGCCACATGCTGGTGTGGCTGACTCTGTAACCTCCCTGCTCATCTGACT 1898
Db 1859 TCTGGTTATTGCTGAGTCTGGGGTGGCTGCTGCTCTCTACTGTCACCTGT 1918
Qy 1899 GCCTGATCTCAGGGGGTGGCTGGGACCAACTGGGGCAGGACAT 1958
Db 1919 GCGCTGATCTCAGGTGCTGAGTCATGCAACAACTGAGCAGGGTTAGGAAC 1978
QY 1959 ACCCTTAAAGAAACTCCAAAGAACCTCCAGTTCACTGCTTATTATAGAACA 2018

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1979 AACCCAGAACAACTCAAGAGAATGTCGATTTCACGGATTATTCACAGTGAACA 2038
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186666
 QY TGTTTCTGCGGTGAAAGTGATTGTTACCTTACTTAGAAAGAGA-----TAT 2072
 PRIOR FILING DATE: 1995-11-12
 PRIOR APPLICATION NUMBER: 60/0653111
 db 2039 TGATTCCTCTGGGAGAACATGATTGATTCATGAGGAGATGGTCT 2098
 PRIOR FILING DATE: 1995-11-13
 PRIOR APPLICATION NUMBER: 60/0667700
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/0759455
 QY 2073 ACAGATTTGCTCATGAGAGGAACTTGTCCTGGCAAGAGATGCGAAATATCAT 2132
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0781000
 db 2099 CTTGATTCCTTATGAAAGCTTGTGACTTGGCCAAAGCATAGTGAATATGT 2158
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0781000
 QY 2113 CAACTGCATGAGAGGAACTTGTCCTGGCAAGAGATGCGAAATATCAT 2192
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0781000
 db 2159 AAGCTCATGAGAAAGCTTATAGTCATCTTGTGTCCTCCAACTTGTCAGAA 2218
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0781000
 Qy 2193 TGAATGGGCCATTAGCAACTTTCATCACAACTCTTCATGAGGATCTAA 2252
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0871066
 Db 2219 TGAGTGGGCCATTATGATTCTACTTGCCACACATCTTCATGAAATTCTGA 2278
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0871066
 Qy 2253 TAACTTAATCTCTACTACTGGACCCATCCAGAACATCATTATGGATTCCA 2312
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0871066
 db 2279 TCACTTAATCTCTACTACTGGACCCATCCAGAACATCATTATGGATTCCA 2338
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0871066
 Qy 2313 CAAGCTGAGGCTCTAGACGGAGGACTTATTGCGAGTGCCTCAAGGAGAAAGCA 2372
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0871066
 db 2339 TAAACTGAAAGCTCTTCAGAAAGACATCTGGATSGCCCAAGGATGGCGFAA 2398
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0871066
 Qy 2373 ACCTGGGGCTTTGGCTAACATTAGCGCGTTTATGAAATAACACTAGTCAC 2432
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0871066
 db 2399 ATCTGGGTTTCGGCAACCTTGAGCTGTTAATGTTATGTTAGCCACAG 2458
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0871066
 Qy 2433 TGAACACATGAGCTGAATCTTAAAAAATTAA 2466
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0871066
 db 2459 AGAAATGTATGACTGCAGACATTCACAGAGTTA 2492
 PRIOR FILING DATE: 1995-02-25
 PRIOR APPLICATION NUMBER: 60/0871066

RESULT 10

US-09-990-444-56

Sequence 56, Application US/09990444

Patent No. 6930170

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerriksen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Klijavín, Ivar J.

APPLICANT: Naper, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730P1C19

CURRENT APPLICATION NUMBER: US/09/990,444

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-15

PRIOR APPLICATION NUMBER: 60/062250

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182

; PRIOR FILING DATE: 1998-07-09

Query Match          28.2%; Score 777.2; DB 3; Length 3462;
Best Local Similarity 59.8%; Pred. No. 3e-209; Matches 1456; Conservatve 0; Mismatches 948; Indels 30; Gaps 8;
Matches 1456; Conservatve 0; Mismatches 948; Indels 30; Gaps 8;

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Qy      105 TTTGTTTGCTTGTATCATATAATGTTGGRACAGAGATCGATGCTCCACGGAAATGA 164
Db      137 ATTTGGTGTAGATGTTGACAGCAGGGTGTGCTCAGAGTCGCAGAGAAGGGA 196
Qy      165 ATTGGAGTAGACAAGCTAAAGGGCTATTCATGTTCCAAGACTTACGCCGCTGA 224
Db      197 ACTGATGACCAACTCTCCACATGCTTCTAGAAAGTGTCCCAGACTGTGCCCCAGC 256
Db      225 ACCAAGAGCTTAGATGTTGACAGACTGAGACTATGCTTAAAGAATCCAGGTC 284
Qy      257 CACAAACACACTGGATTATCTTAACTCCCTTCACTCCAGAGTTCA 316
Db      285 CTTCATCATGAGTTGACAGTTGAGCTTCCATAAACAGAAATCCAGACTGTT 344
Qy      317 TTCTGTCCTCAAATCTGAGAGTTGTCTATGCCATAAAGAAATTCAGCT 376
Db      345 AAGTGTTCAGTCAGTCACCGGATTAGATTTGGATTATTCATATCAGTTGA 404
Qy      377 CAAACCTTCAATCACACAGGTTAAATTTGATTGTTGCTTAAACAGTGA 436
Db      405 AAAGATTCCTGCCATCTTGTGAGTTGGCAACTTACACATGTTCTTAAAGT 464
Qy      437 GAGTGTGACTGGTATTACTGGCAGGCTCAGGTTAGATCTTAAAGCT 496
Db      465 CAAGGCCCTGSCCACTGTGAGATTGGCAACTTACACATGTTCTTGGATT 524
Qy      497 TCAACCATGCTATCTGAGGAACCTGACCTGGAACTCTTCTTAAAGT 556
Db      525 GAGTGTCTGAGCTCCAAATTAGTTGCTGCTCAATGCTCACTGCTATGTTA 584
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Db      585 TATCCCTCTGGATTAGAAATTATATAAAAGAAAGAGAGAGAGAGAGAAT 644
Qy      617 TGTCTCTCTGGATTGAGCTCTCTCT---CATATGAGAGGGTAGCTGCCAT 670
Db      645 TCTGAAAGCAAAACCCCTCACCTGTTTCACCCAACTGTTTATCTCTCAAGT 704
Qy      671 CTAAACACAAACTGACATGTTACCAATGACAAATTCGGTCTTT 730
Db      705 GAACATTCAGTAACTTCTAGGCTCTACACTGACTAATTAATGAAATGTA 764
Qy      731 GCGTGTGAACTCAACCTCAAAATATAGAAATGACACATA-TAGATGCAAGGC 789
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Db	848	TCTATGCTTTAATAGTTGATTTACTCTGGGACACTTCAGATGGAACTTCACTTCAACTTGT	907	Db	1919	Gccctgatatttcggatgtcttaggtcatgcacacaatgcacagggttaggaac	1978		
Qy	885	TGGCCCAAACCTGTGAAATCTCAATTACAATTAAACATATTGAAAGCATTCG	944	Qy	1959	ACCTTGGAGAACTCCAGAACCTCCAGTTGAGCTTATTCATAGTGACCA	2018		
Db	908	TGGCATACATCACTAGTGGACACTTCAGATCCGAAATGTGAGTTGGTAGGCTA	967	Db	1979	AACCCAGAAACTCAAGAATGTCGATCCGATTCAGCACTACAGTGACAGACA	2038		
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Db	968	TCTTGACCAATCATTTGACTACTCAATAGTAACTGAGAACTATAATTGGAGCA	1027	Db	2039	TAATCTCTGGGAGAGTGAATGTCACCCAACTTAGAGAGAAGTGGTCTAT	2098		
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Qy	1659	CCAATGAACTGTGAGTAAAGAATTAGCAAGTATCACTGAGT	1718	; APPLICANT: Desnoyers, Luc					
Db	1682	CGCGTGTACTCTGAAACTTATGAGCTGATGAGCTCAT	1738	; APPLICANT: Eaton, Dan L.					
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Qy	1779	ACTAAAGGACTTCACATGTCGAATATCTGCAACATACTCGTGTGTCACCAT	1838	; APPLICANT: Gerber, Hanspeter					
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; APPLICANT: Williams, P. Mickey									
; APPLICANT: Wood, William I.									
; APPLICANT: Zhang, Zemin									
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic									

TITLE OF INVENTION: acids Encoding the Same
FILE REFERENCE: P2730AC27
CURRENT APPLICATION NUMBER: US/09/997,333
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-06-25

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 Db 2399 ATGGGGCTTCTGGCACACCTCGAGCTGCTTAAATGTTAATGTTAATGACCG 2458
 Qy 2433 TGAACACAAATGATGAAATTAAATTA 2466
 Db 2459 AGAATGATGAACTCGAGATTCTCGAGTTA 2492

RESULT 12
 US-09-992-598-56 Application US/09992598
 ; Sequence 56, Application US/09992598
 ; Patient No. 6956108

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watnabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zenin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C20

CURRENT APPLICATION NUMBER: US/09/992,598

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-05-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

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 Db 617 TGTCTCTCTAGATTCAGACACTCTCT---CATTAGAGAGGTGCGCTGCCAT 670
 QY 645 TCTGAATGCAAAAACCTTCCTCGCTGTTTACCCACTAGTTATCGGTATCCAAT 704
 Db 671 CTTAACACACAACAACTGCACTGTTACCAATGACACAATTCTGGTCTTT 730
 QY 705 GAAACATATCAGTTAACTTAGGGGCTTCAACTGACTATATAATGAGATGATGA 764
 Db 731 CGGTGATGGAAACAGACTTAAACATGACAATA-TAGATGCAAAAGCC 789
 QY 765 CAACTCTCAAGTTCTAAATTATCAGACTCACAGAGGTCAACCTACTGAA 824
 Db 790 ATTGTTAAGTTATGAAATGCAAGAACTTGTGTTAGAAATGCTAAGC--ATGGT 847
 QY 825 TTACCTCACCACATAGAAACAGACTTAAATATTAGAAATGACAATA 884
 Db 848 TCTATGCTTAAATAGTGAATTACTCTGGGAGACCTTCTTACTACAATTGT 907
 QY 885 TTGGCCAACACTGGAATTCTCAATATTACAAATTAAATGAAAGCATTCG 944
 Db 908 TTGGCATACATCAGTGAACTTCTCAGATCGAAATGAGCTTAAGCTTA 967
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 QY 999 TATCAGGAAACAGTTTCTGTTACAGACATAATGTTGAGAT 1058
 Db 1028 TGTACATTCTAGAGTGTAACTTACATCACAGATAAACTTGTGAGAT 1087
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 QY 1179 AAATGTTCCAGTGTAACTTACATCACAGATAAACTTGTGAGAT 1238
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 QY 2019 TGATCTGCTGGGAAAGTGAATTGGAACCTTACCTGAAAGAGA----TAT 2072
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 QY 2253 TAACTTATCCTCATTTACTGGAAACCCTCCACAGAACAGCATTCCTAACAGTAA 2312
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 QY 2313 CAAGTGAAGGCTCTGACGAGGGACTTATGAGCTGGCCCAAGGAAAGCAA 2372
 Db 2339 TAACTGAAAGCTCTCTGGAAAAAAAGCTACTGATGAGTGGCCAAAGATGGCTAA 2398
 QY 2373 ACCTGGGCTTTCGGCTACATGAGGCGCTTATGAGAAATGACTGTCAC 2432
 Db 2399 ATGGGCTTTCGGCAACCTGGAGCTGCTTAACTGATGTTAGCCACAG 2458
 QY 2433 TGAACACAACTGAGAACTTAAAGAAATTAA 2466
 Db 2459 AGAAATGATGACTCAGACATCACAGAGTTA 2492

RESULT 13
 US-09-989-735-56
 ; Sequence 56, Application US/09999735
 ; Patent No. 6372185.
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P27301PC61

CURRENT APPLICATION NUMBER: US/09/989,735

CURRENT FILING DATE: 2001-11-19

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PRIOR FILING DATE: 1997-06-16

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PRIOR FILING DATE: 1997-11-12

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PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/065770

PRIOR FILING DATE: 1997-11-24

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PRIOR FILING DATE: 1998-02-25

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RESULT 14

US-09-989-726-56

; Sequence 56, Application US/09989726

; Patent No. 7,018811

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

Db 1562 CAGTCATTCTAGTAGACTTCACTCTGAAATGAACTTCATGCCATC 1621 ; APPLICANT: Eaton, Dan L.

Qy 1599 GGCTGATTCTCCAGAGCTGCAGAAGATGAGGTCAAATAAAGCAGGGACATCATT 1658 ; APPLICANT: Ferrara, Napoleone

Db 1622 TCGGATTTGTCAGACTGCAGGAGTTAAACTCTAAATGCGGAAGAACATT 1681 ; APPLICANT: Fong, Sherman

Qy 1659 CCATGATGACTCTGTGAGCTAGAGAAATTGTCAAATAATAGCCAGSTATGAGT 1718 ; APPLICANT: Gerber, Hanspeter

Db 1682 CGCGTGTACCTGGAATTA---AAATTCTCATCAGCTGAGAACATTCAGGGTCAT 1738 ; APPLICANT: Gerrissen, Mary E.

Qy 1719 GTTGTAGAGGGTGCGCTGATTTCTATAAGTGTACTACCCAGGAAGTTAGAGGAAGCCC 1778 ; APPLICANT: Goddard, Audrey

Db 1739 GATGGTTGATGGTCAGATTCATACACTCTGTGATACTACCTTAACCTTAAGGGAACTAG 1798 ; APPLICANT: Grimaldi, J. Christopher

Qy 1779 ACTAAAGACTTCACATGTCGAAATTCTCCACAATACTCTGTGATGTCACCAT 1838 ; APPLICANT: Guney, Austin L.

Db 1799 GTTAAAGAGCTCATCCAGAAATTCTGCAACAGCCTGTCGTTGAGGTCAAT 1858 ; APPLICANT: Kijavrin, Ivar J.

Qy 1839 CGGTGCCCCATGCTGGGTGCTGTGACTGTGACCTGACCTCCTGCACTACTGGATCT 1898 ; APPLICANT: Napier, Mary A.

Db 1859 TGTGGTATTATGCTAGTCTGTGCGGTGCTGTCGCTTCGTCCTTGATCT 1918 ; APPLICANT: Pan, James

Qy 1899 GCCTGTTATCTCAGGGTGTGCTGACCTGACCTCCTGCACTACTGGATCT 1958 ; APPLICANT: Paoni, Nicholas F.

Db 1919 GGCCTGGTATCTCAGGGTGTGCTGACCTGACCTCCTGCACTACTGGATCT 1978 ; APPLICANT: Roy, Margaret Ann

Qy 1959 ACCCTAGAGAACTCCAGAACGAAACTTGTACCTTACCTTATTCATAGTAGTGAAC 2018 ; APPLICANT: Stewart, Timothy A.

Db 1979 AACCCAGAACACTCAAGAAATGTCGCACTCCACCTAGAGAACATTGTCAT 2098 ; APPLICANT: Tumas, Daniel

Qy 2019 TGATTCGCTCTGGTGAAGAATGGAATGGTACCTTACCTAGAAAGAGA-----TAT 2072 ; APPLICANT: Watanabe, Colin K.

Db 2039 TGATTCCTGTCGGTGAAGAATGTCATGATCCCACTTAGAGAGGAATGTTCTAT 2132 ; APPLICANT: Williams, P. Mickey

Qy 2073 ACAGATTGTCTTCATGAGAGCACTTGTGCTGGAGACATGTGGAAATATCAT 2132 ; APPLICANT: Wood, William I.

Db 2099 CTGTGATTGCTTATGAAAGCTACTTGTACCTGACCTTGTCCTGGCAAGAACATTAGTGAATATTGT 2158 ; APPLICANT: Zhang, Zemin

Qy 2113 CAACTGATTCAGAGGTTTACAGTCATCTGTTGTCCTCCACTTGTGTCAGAG 2192 ; TITLE OF INVENTION: Acids Encoding the Same

Db 2219 TGAGTGGTGCATTATGAAATTACTTGTGTCATCTGTCATCTGTCATGAAATTCTGA 2278 ; FILE REFERENCE: P2730PC60

Qy 2253 TAATCTTATCTCATCTTACTGAAACCATTCCACAGCAACGCAATTCCACAACTTACCA 2218 ; CURRENT APPLICATION NUMBER: US/09/989,726

Db 2279 TCATATATTCTTATCTTACTGAAACCATTCCATCTTATGCACTCCACAGGTATCA 2338 ; PRIOR FILING DATE: 1997-11-19

Qy 2313 CAACTGAGGCTCTCTGAGCCAGCGACTATTGAGGGCCAAAGGAAAGCAA 2372 ; PRIOR FILING DATE: 1997-06-16

Db 2339 TAATCTGAAACTCTCTGGAAAAAAAGCTACTTGTGAATGGCCAAAGGATAGSGTAA 2398 ; PRIOR FILING DATE: 1997-06-13

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Qy 2433 TGAACACAAATGTTGTTAATCTTAAAAAATTA 2466 ; PRIOR FILING DATE: 1998-02-25

Db 2459 AGAAATGTTACTGAGACATTCAACAGGTTA 2492 ; PRIOR FILING DATE: 1998-05-07

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; PRIOR APPLICATION NUMBER: 60/090444

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Query Match 28.2%; Score 777.2; DB 5; Length 3462;

Best Local Similarity 59.3%; Pred. No. 3e-209; Mismatches 948; Indels 30; Gaps 8; Matches 1456; Conservative 0;

Qy	45	TAGGATAGCCACTGCACATCATGCCAACAGAACCTATGTGTTAAAGCTTCA	104
Db	77	TGAGGAATAAGTGTTAAATCCTGGAAATACATGAGTCAT	136
Qy	105	TTTGTGCTTATGATCATATAATGTTGGACAGAGTCAGTCTCCGACGAAATGA	164
Db	137	ATTTGCTGATATTGTATGACGAGGAGGTGATGCTCCAGAGCTGAGCTGAGAAGAGGA	196
Qy	165	ATTTGCGTAGACAAGTCAAAGAGGCTTATTCATGTCACAAAGACCTACCGCTGA	224
Db	197	ACTGATCACCAACTGCTCCACATGTCAGAAGGTTCCCGAGACTGACCCAGC	256
Qy	225	AACCAAGTCTAGATGATGCTGAGAACATACATCCTGAGCTTGGTCCTGACATGAG	284
Db	257	CACAAAGCACTGGATTATCTTAAACCTCTTTCACAGAGTCAGTTCA	316
Qy	285	CTTCATCAGAGTTCAGTTGAGCTTCCATACAGAACTCCAGTACTGTATT	344
Db	317	TCTGCTCCACAGAGTTGATCTATGCCATAACAGAATTCACAGCTGATCT	376
Qy	345	AAGTGTTCAGTTGACCAAGGTTAGATAATTGATTATCTCATACAGTTGA	404

Db	377	CAAAACCTTGAATCAACAGGAGTTAGATAATTAGATTCAGTCAAGACAGAA	436	Db	1442	TATCAAACTTGACCTTAATAACCAATCCAACTGTACTAAGAGACTATCA	1501
Qy	405	AAAGATATCCTGCATCCTATGTGAGTTAGCGCATTTGATCTCTCATCATGTT	464	Qy	1479	ACTGGAGACTTGCAAGAACACTCAATGTGCTTCATCTTAACTGACCTCCGGATG	1538
Db	437	GACTGTACTTGTGTTTACTTGTGAGCTCAGGTTAGATGCTTGTGAGCTT	496	Db	1502	TCTGATGCGCTTACGACAACTAAATATGCAATTATTTCATGACTATCCTCGGATG	1561
Qy	465	CAAGGCCCTGCCATCTGTAAGGAAATTGGCAACTTACAACTGAAATTCTGGATT	524	Qy	1519	TGGCAGCTTAGGAGCTCAGTGTGATGATGATGATGAGATGACTCTCTCAGCCATC	1598
Db	497	TGACACCAGCTTACGTGAGGAGCTGGCACATGTCACCTGGAAATCTTAGGTT	556	Db	1562	CAGTCATTCAGTAGCTTGTGACTTGTGACTGAACTTGTGATTAATTCAGGTT	1621
Qy	525	GAGTGCTATGAGCTGCAAATACTAAATCAGATTCCAGAAATTGCTCACTGATC	584	Qy	1599	GCGTGTATTCGAGGCTGAGAGATGAGGCTATAAAAGCAGGGAAATCATT	1658
Db	557	GAGTGGGCAAAATACTAAATCAGATTCCAGAAATTGCTCACTGATC	616	Db	1622	TCTGGATTITGTCAGCTGCGCAGGAGTAAACCTCTAAATGCGGAAATTCATT	1681
Qy	585	TATCCTCTGAGTTAGAAATTATATATAAGAAATGAGACAGAGAGCTCAAAAT	644	Qy	1659	CGAACTGACTCTGAGGTTAGAAATTGTGCAAAATAATGAGCAGGAGTCAAGT	1718
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Qy	645	TCTGAATGCAAAACCCCTCACCTGTTTCAACCAACTGTTTCACTGAACT	704	Qy	1719	GTTAGAGGGCTGCTTCTATAGTGTGACTACCCAGAAAGTTATAGGGAGCCC	1778
Db	671	CTTAACACAAACAACACTGCACATGCTTCTTCTTCTTCTTCTTCTT	730	Db	1739	GATGGTGTGAGTGTGAGATCTACACTGAACTTGTGAACTTGTGACCAT	1798
Qy	705	GIACATATGAACTTAACTTGTGTTTACACTGAACTTAAATTAATGATGAA	764	Qy	1779	ACTAAAGAGCTTCAATGTCAGTGTGAAATTATCTTGCAACAACTACTGTC	1838
Db	731	GGCTGATGATGAACTCAAGCTTCAAAATATGAAATGACAATA-TAGATGCAAAAGCC	789	Db	1799	GTTAALAGAGCTTCAGGAGTAAACCTCTAAATGAGGAAATTCATT	1858
Qy	765	CAACTGTCAGTTTCAATAATTTCAGACTCAGCAGAACTTGTGAAATGCA	824	Qy	1839	CGGTGCCCCATGCTGTTGGCTGACTGTGACCTCCCTGATCTACTGGAT	1898
Db	790	AATTGTTGAACTTGTGAAATGCAAGAACTTGTGAAATGCA-ATGGT	847	Db	1859	TGTGTTATTATGCTAGTGTGTTCTGGGGTGGCTGCTGCTGCTGACTTGACT	1918
Qy	825	TTTACCTCACCACATAGAAACGACTTGGAATGCTGCTCAGACTCTTCATTCT	884	Qy	1899	GCCCTGGTATCTCAGGGGGTGCGGTGAGGACACTGGGAGGGCCAGGACAT	1958
Db	848	TCTATGCTTAAATAAGTGTGTTACTCTGGSAGACCTTCTTCTTCTTCAATTGT	907	Db	1919	GCCCTGGTATCTCAGGGTGTGACTGTCAGTGTGAACTGACACAGCTGTC	1978
Qy	885	TGGCCCAAAACCTGTCGATCTCAATAATTCAAAATTAATGAACTTGTGAGCT	944	Qy	1959	ACCTTGAGAGACTCCAAGAAACCTCCAGTTCTGTTTATTCATATAGCA	2018
Db	908	TGGCATACATGTCAGACCTTCAGATCGAGCTTGTGAGCTTGTGAGCTTGT	967	Db	1979	AACCCAGAACTCAAGAGAAATGTCGATTCAGGAACTTGTGAGCTTGTGAGCT	2038
Qy	945	TGAGAGA-----TTTACTTAACTCAAAAGACATGGAGGATGAGAGATGAGA	998	Qy	2019	TGATTCGGCCCTGGGGAAGTGTGAACTTACTAGAAAMAGAGA-----TAT	2072
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Qy	999	TATCAGGAAACCAAGTTCTGTTCAACAGACGTTGTGACCTGTTCTGAGAT	1058	Qy	2073	ACAGATTGTCTCATGAGGAACTTGTGCTCTGGAGAGCATGTGGAAATATCAT	2132
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Qy	1179	AAATGTTCCACGTTAGTTAAATTGGAGACACTTACAAATAATGTTAAAGA	1238	Qy	2253	TACTTATCCTCATCTACTGGAAACCATTACAGACAGCATCCACAGATCA	2312
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Qy	1239	CCTTTCAAACTGGTCTCATGAGGAGATGCCCTTGTGAAATACGTGTTAG	1298	Qy	2313	CAAGCTGAGGCTCTCATGAGGAGCTTGTGAGGAGCTTGTGAGAAGCAA	2372
Db	1268	ACTTCCTTAACTGAGTGTGCTTGTGAGACACCTGAGCTG	1324	Db	2339	TAACCTGAAACTCTCTGGAAAGGATACTTGTGAGTGGCCACAGGATGGCTAA	2398
Qy	1299	CTGGAATCTCTGAACTCTGGAGACATGAGAAACTCTGCTCTGGTGTGAGAGT	1358	Qy	2373	ACGTGGCTTGTGAGGAGCTGCTTGTGAGTAACTGAGCTGCTTGTGAGT	2432
Db	1325	TGAAATCTTACAAAC---ATAAAATGAGAAATGTCGATGAGGACTGTG	1381	Db	2399	ATGGCTTGTGAGGAGCTTGTGAGTAACTGAGCTTGTGAGT	2458
Qy	1359	GCTGTTAACTGCTCAATAATGCTGACTGCTGTTGTGAGCTCCAG	1418	Qy	2433	TGAACAACTGAGGAACTTAAAGATTA	2466
Db	1382	CAATATGAACTGTCATCAATAATGTCGATGCTGAGGCTGCCCAGA	1441	Db	2459	AGAAATGTTGAGGAGCTCACAGAGTTA	2492
Qy	1419	GATCAAGTGTGAGGAGCTAACAGCTGCTAA	1478				

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; Sequence 56, Application US/09997514
; Patent No. 701915
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavine, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 28.2%; Score 777.2; DB 5; Length 3462;
Best Local Similarity 59.8%; Prc. No. 3e 209; Matches 1456; Conservative 0; Mismatches 948; Indels 30; Gaps 8;

Qy      45 TAGGTTAGCCACTGCAACATCATGCCAACAGAACATTATGTTAAAGCCTTCA 104
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Qy      285 CTTCCTATCAGTGTGACAGCTTGTGACTTTCCTAACAGAACCTCCAGTACTGTGTT 344
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b	1959	ACCTTGAAGAACTCCAAGAACCTCGAGTTCATGCTTTATTCATAGGAA	2018
b	1979	AACCCAAAGAACACTCAAGAGAAATGTCGGATTCACGGATTATTCTACAGTCACAA	2038
b	2019	TGATCTCCTGGTGAAGAAGTGTGATTGGTACCTTACCTAGAAAGAAGA-----TAT	2072
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b	2253	TACTTATCTCATCTACTGGACCCATTCCAGAACAGCATTCACAGAACATCTTCATGAAATTCTGA	2312
b	2279	TCATATTAATTCTCATCTACTGGACCCATTCCATTTAGTGTGTTAGGACCCAG	2338
b	2313	CAAGCTGAGGGCTCATGACCGAGGGAAATTGTCAGTGGCCAAAGAAAGCAA	2372
b	2339	TAAGCTGAAAGCTCTCTGGAAAAAAAGCATACTTGTGAAATGGCCCAAGGATGGCTAA	2398
b	2373	ACGTGGGCTTGGCTAACATTAGGGCCTTTAATGAAATTAACTAGTCAC	2432
b	2399	ATGTGGCTTGGCTAACCTCTGAGCTGAGTCATTGAACTTGTGTTAGGACCCAG	2458

DR	SMR; Q9Y2C9; 630-786.	QY	61 QNYIAELQYSDMSFSELTVELRSHNRQLDLSVFKENOLETLDSHNOLOKISCHP 120
DR	Ensembl; ENSG00000174130; Homo sapiens.	Db	61 QNYIAELQYSDMSFSELTVELRSHNRQLDLSVFKENOLETLDSHNOLOKISCHP 120
DR	HGNC; HGNC; 16711; TLR6.	QY	121 VSFRHLDLSNDKFALPKICKERGNLSQLNPLGSAMKQDLPPIAHHLSSYLDRN 180
DR	MIM; 60503; gene.	Db	121 VSFRHLDLSNDKFALPKICKERGNLSQLNPLGSAMKQDLPPIAHHLSSYLDRN 180
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.	QY	181 YYIKENETTSLOQINAKTTHLVFAHTSLAIQVNISVNTIGCQLQINNKLANDNCQFIR 240
DR	GO; GO:0016020; C:nembrane; ISS.	Db	181 YYIKENETTSLOQINAKTTHLVFAHTSLAIQVNISVNTIGCQLQINNKLANDNCQFIR 240
DR	GO; GO:0045335; C:phagocytic vesicle; ISS.	QY	241 FLSLETGRGSTLNFTNLHETTWICLVRUFOFLBPKPVSYLNTNLIESIREBDFTS 300
DR	GO; GO:0008034; F:ipoprotein binding; ISS.	Db	241 FLSLETGRGSTLNFTNLHETTWICLVRUFOFLBPKPVSYLNTNLIESIREBDFTS 300
DR	GO; GO:004888; F:transmembrane receptor activity; ISS.	QY	301 KTKLALKTEHTINQVFLSQTAIYTVESEMINTLTSDFPFIHMLCHAPSTFKFN 360
DR	GO; GO:007250; :activation of NF-kappaB inducing kinase; NAS.	Db	301 KTKLALKTEHTINQVFLSQTAIYTVESEMINTLTSDFPFIHMLCHAPSTFKFN 360
DR	GO; GO:0042742; P:defense response to bacteria; TAS.	QY	361 TQNVTIDSIFEKCSITLVKLETLIQKNGKDUFKGWLTQKMPSELIVLWSMSGRH 420
DR	GO; GO:009598; P:detection of pathogenic bacteria; ISS.	Db	361 TQNVTIDSIFEKCSITLVKLETLIQKNGKDUFKGWLTQKMPSELIVLWSMSGRH 420
DR	GO; GO:006955; P:immune response; TAS.	QY	421 KENCTTWESTVWLNSNMILTSVERCLPRKYLDEHENKIKSVPKQVKLAEQELAV 480
DR	GO; GO:0042116; P:macrophage activation; ISS.	Db	421 KENCTTWESTVWLNSNMILTSVERCLPRKYLDEHENKIKSVPKQVKLAEQELAV 480
DR	GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . ; ISS.	QY	481 AFNSUTDLPGCSFSSLVSLIDNSVSPSADPQSCOKRS-TKAGDNPFOCTELREF 540
DR	GO; GO:007165; P:signal transduction; TAS.	Db	481 AFNSUTDLPGCSFSSLVSLIDNSVSPSADPQSCOKRS-TKAGDNPFOCTELREF 540
DR	GO; GO:0042488; P:T-helper 1 type immune response; IC.	QY	541 VKNIDQVSSEVLEGWPSYCKDPSYRSPLKPHMSELSNCNTLTVTIGATMLVLAV 600
DR	GO; GO:004075; IL1_rcpt_1.	Db	541 VKNIDQVSSEVLEGWPSYCKDPSYRSPLKPHMSELSNCNTLTVTIGATMLVLAV 600
DR	InterPro; IPR001611; LRR.	QY	601 TVTSCICRYLDPWYRWCWOTERRARNIPBLQRNQFHAFISYSBHDSAWKSEL 660
DR	InterPro; IPR000483; LRR_C.	Db	601 TVTSCICRYLDPWYRWCWOTERRARNIPBLQRNQFHAFISYSBHDSAWKSEL 660
DR	InterPro; IPR03591; LRR_typ.	QY	661 UPYLECDIOLCLHERNFPVGKSVIENINIEKSYKSIFVLSNFVQSBWCHYELYFAH 720
DR	InterPro; IPR00157; INTRINXIRIF.	Db	661 UPYLECDIOLCLHERNFPVGKSVIENINIEKSYKSIFVLSNFVQSBWCHYELYFAH 720
DR	PRINTS; PR00019; LERICHIRPT.	QY	721 HNLFHFGNNLILIPITFONSTINKYKUKALMTQRTYIQLWPKEXSKRGLFWANIRAA 780
DR	SMART; SM00082; LRR_T; 1.	Db	721 HNLFHFGNNLILIPITFONSTINKYKUKALMTQRTYIQLWPKEXSKRGLFWANIRAA 780
DR	SMART; SM00255; TIR; 1.	QY	781 FNMKLTIVTENDVKS 796
KW	PROSITE; PS50104; TIR; 1.	Db	781 FNMKLTIVTENDVKS 796
KW	Glycoprotein; Immune response; Innate immunity;	QY	781 FNMKLTIVTENDVKS 796
KW	leucine-rich repeat; Membrane; Receptor; Repeat; Signal;	Db	781 FNMKLTIVTENDVKS 796
KW	Transmembrane.	QY	781 FNMKLTIVTENDVKS 796
FT	CHAIN	1	Potential.
FT	CHAIN	32	Toll-like receptor 6.
FT	TOPO_DOM	32	/FT-ID-PRO_0000034731.
FT	TRANSMEM	586	Extracellular (Potential).
FT	TOPO_DOM	587	Potential.
FT	REPEAT	608	Cytoplasmic (Potential).
FT	REPEAT	74	LRR 1.
FT	REPEAT	75	LRR 2.
FT	REPEAT	100	LRR 3.
FT	REPEAT	121	LRR 4.
FT	REPEAT	158	LRR 5.
FT	REPEAT	176	LRR 6.
FT	REPEAT	222	LRR 7.
FT	REPEAT	376	LRR 8.
FT	REPEAT	402	LRR 9.
FT	REPEAT	430	LRR 10.
FT	REPEAT	449	LRR 11.
FT	REPEAT	474	LRR 12.
FT	REPEAT	498	LRR 13.
FT	DOMAIN	517	TIR.
FT	CARBONYD	144	N-linked (GLCNAC. .) (Potential).
FT	CARBONYD	186	N-linked (GLCNAC. .) (Potential).
FT	CARBONYD	214	N-linked (GLCNAC. .) (Potential).
FT	CARBONYD	253	N-linked (GLCNAC. .) (Potential).
FT	CARBONYD	285	N-linked (GLCNAC. .) (Potential).
FT	CARBONYD	359	N-linked (GLCNAC. .) (Potential).
FT	CARBONYD	423	N-linked (GLCNAC. .) (Potential).
FT	CARBONYD	434	N-linked (GLCNAC. .) (Potential).
FT	CARBONYD	583	N-linked (GLCNAC. .) (Potential).
SQ	SEQUENCE	796 AA;	91890 MW; -35CAEAC05BBFABBD CMC64;
Query Match	Best Local Similarity	99.9%	; Score 4149; DB 1; Length 796;
Matches	795; Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
QY	1 MTKDKRPIVKSFHFVCLMIIVGTRTOFSDEMEFAVDSKSKRLIHVKDPLPKTYLDMS	RN	[1]
Db	1 MTKDKRPIVKSFHFVCLMIIVGTRTOFSDEMEFAVDSKSKRLIHVKDPLPKTYLDMS	RN	[2]

NUCLEOTIDE SEQUENCE

Shinkai H., Uenishi H.;

"Coding sequence of porcine TLR6."

Submitted (Mar 2005) to the EMBL/GemBank/DDJB databases.

RP NUCLEOTIDE SEQUENCE.
 RA Shinkai H.; Uemishi H.;
 RT "Nucleotide sequence of porcine genomic region containing TIR1, TLR6
 and TLR10";
 RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.

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DR EMBL; AB208698; BAD1801_1; -; Genomic_DNA.
 DR EMBL; AB210286; BAD3713_1; -; Genomic_DNA.

DR SMR; 059H16; 630-785;
 GO; GO:0016020; C:membrane; IBA.
 GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR InterPro; IPR01611; LRR.
 DR InterPro; IPR00483; LRR_C.
 DR InterPro; IPR003591; LRR_TYP.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF00560; LRR_1; 7.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR_1.
 DR PRINTS; PR01537; INTRUKNIR1F.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR_1.
 DR PROSITE; PSS0104; TIR; 1.
 KW Receptor.
 SQ SEQUENCE 796 AA; 91460 MW; 8CE2A2375606CA55 CRC64;
 Query Match 81.2%; Score 3374; DB 2; Length 796,
 Best Local Similarity 79.4%; Pred. No. 2.4e-202;
 Matches 632; Conservative 77; Mismatches 87; Indels 0; Gaps 0;
 DR 1 MTQDKKEPIVKSFHFVCLMILIVGTRIQPSDNEFAVDKSKGGLIHVPKDLPLKTKVLDS 60
 DR 1 NSKDKKEPIVTISLHSVVWMLWWTGTLIQFSESEFVUDSKSGLIGLRTVPKDPLPQTKVLDV 60
 DR 61 QNYIAELQVSMSFSLSEBLTVERLSHRIQLDLSVFKFNOLDEYLDLISHNQLOKISCHPI 120
 DR 61 QNFITELHLSDISFLSISQLTQVRLRSLQNMQCLIDSVFKFNQDLEYLDLISHNQLOQTLCHPI 120
 DR 121 VSPRHDLDFNDPKALPICKERFGNLSQLNFGISAMKQKDLPLTAHJHSYIULRN 180
 DR 121 TSKLHDLSFNDPEALPICKERFGNLSQLNFGISAMKQKDLPLTAHJHSYIULRN 180
 DR 181 YYIKENETESTQILNAKTLHTVFHPTSLFLATQVNLSVNTLGCLQLTNKUNDNCQFIK 240
 DR 181 YYMKENEKESEQIQLINTKQKUHVPHENNSFFSQVNISVKSVCQCLQANIKSDDNCOVFT 240
 DR 241 FLSLELRGTSILNFTNHIEFWKCLVRYFQFLPWRPEVEYNINYNTIESIREDFFTS 300
 DR 241 FILLELTQGQPTILNFTNHIEFWKCLVGFQFLPWRPEVEYLIVNLTIVESIDEDEDFYY 300
 DR 301 KITKLKALTEHTINQVPLFSOTALLYFVSEANIMMITSDFPFIHMLCPHPASTKFELNF 360
 DR 301 ETTLKQVKIEHTKRVFIFQSTALYRVSDFNIMRITIADPHIHLCPQPVSTENFLNF 360
 DR 361 TQNVFTDSIFFRKCASTLVKLETILQOKNLQKLFKVGMKTQMSPLETDYWSNSLIESGRH 420
 DR 361 TQNVFTDSIFFRKCASTLVKLETILQOKNLQKLFKVGMKTQMSPLETDYWSNSLIESGRH 420
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR01537; INTRUKNIR1F.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PSS0104; TIR; 1.
 KW Receptor.
 SQ SEQUENCE 796 AA; 91414 MW; 36C489D2CC339F81 CRC64;
 Query Match 80.9%; Score 3361; DB 2; Length 796,
 Best Local Similarity 79.1%; Pred. No. 1.6e-201;
 Matches 630; Conservative 77; Mismatches 89; Indels 0; Gaps 0;
 DR 1 MTQDKKEPIVKSFHFVCLMILIVGTRIQPSDNEFAVDKSKGGLIHVPKDLPLKTKVLDS 60
 DR 1 NSKDKKEPIVTISLHSVVWMLWWTGTLIQFSESEFVUDSKSGLIGLRTVPKDPLPQTKVLDV 60
 DR 541 VKNQDQVSSELEGWDPSYKDPESYRGSPSKDPMSELSCNITLIVTGATMVL 600
 DR 541 IOSLGQVSSDVESWPDSYECPYEPESYKGTLIKDFRVSLECNNTALLIVTGTGVLAL 600

QY RESULT 3
 QY 076L23_PIG PIG PRELIMINARY; PRT; 796 AA.
 QY 076L23_PIG PIG PRELIMINARY; PRT; 796 AA.
 QY 076L23_PIG PIG PRELIMINARY; PRT; 796 AA.
 DR 05-JUL-2004, integrated into UniProtKB/TREMBL.
 DT 05-JUL-2004, sequence version 11.
 DT 07-FEB-2006, entry version 11.
 DE Toll-like receptor 6.
 JN Name=TLR-6;
 OS Sus scrofa (pig).
 OC Bubaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus. Sus.
 RN NCBI_TaxID=9823;
 RN [1]-
 RP NUCLEOTIDE SEQUENCE.
 RR MEDLINE=22948431; PubMed=14585198; DOI=10.1089/10799003322485080;
 RA Munera Y., Uemishi H., Kikuma R., Yamamoto R., Hamashima N., Yokomizo Y., Mori Y., Shimoji Y.,
 RT "Porcine TLR2 and TLR6: identification and their involvement in Mycoplasma hyopneumoniae infection." In: J. Interferon Cytokine Res. 23:583-590(2003).
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DR AB005936; BAC09317_1; -; mRNA.
 DR SMR; 076L23; 630-785.
 DR GO; GO:0016020; C:membrane; IBA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR00488; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR00157; TIR.
 DR InterPro; IPR00351; LRR_TYP.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR01537; INTRUKNIR1F.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PSS0104; TIR; 1.
 KW Receptor.
 SQ SEQUENCE 796 AA; 91414 MW; 36C489D2CC339F81 CRC64;
 Query Match 80.9%; Score 3361; DB 2; Length 796,
 Best Local Similarity 79.1%; Pred. No. 1.6e-201;
 Matches 630; Conservative 77; Mismatches 89; Indels 0; Gaps 0;
 DR 1 MTQDKKEPIVKSFHFVCLMILIVGTRIQPSDNEFAVDKSKGGLIHVPKDLPLKTKVLDS 60
 DR 1 NSKDKKEPIVTISLHSVVWMLWWTGTLIQFSESEFVUDSKSGLIGLRTVPKDPLPQTKVLDV 60
 DR 1 NSKDKKEPIVKSFHFVCLMILIVGTRIQPSDNEFAVDKSKGGLIHVPKDLPLKTKVLDS 60

Db	61 QNPITEHLISDSFLSQTIVLRLSRQCLDSVFKENQDLYIDLSHNLQOTLCHPI	DR	EMBL; AU620670; CAE06197.1; -; Genomic_DNA.
Qy	121 VSFRHLDLSFNDPKALPICKERFENLSOLNPLGLSAMKLUQDLIPTIAHLSYTLDLRN	DR	SMR; Q704V6; 630-789.
Db	121 TSLKLHDLSPNDFEALPICKERFENLTSOLNPLGLSAMKLUQDLIPTIAHLSYTLDLRN	DR	Ensembl; ENSPAG0000014031; Bos taurus.
Qy	181 YYIKENETESLQINAKTILVLFHPTSLFAIQNISVNTLGCLQLTNLKNDNCQVFI	DR	GO; GO:0015020; C-membrane; IEA.
Db	181 YYIKENETESLQINAKTILVLFHPTSLFAIQNISVNTLGCLQLTNLKNDNCQVFI	DR	GO; GO:0004888; Filtratransmembrane receptor activity; IEA.
Qy	241 FASLBUTRSTLLAFTNLHIEITWKLVLVRVQFLMPKPEYLNLYNTIESIRBDFTY	DR	InterPro; IPR001611; IRR.
Db	241 FASLBUTRSTLLAFTNLHIEITWKLVLVRVQFLMPKPEYLNLYNTIESIRBDFTY	DR	InterPro; IPR00483; LRR_C.
Qy	301 KTTKLALKTIEHTINQVLFPSQTLTYTVFSEMNIMLTSIDTPFTHMLCPHARSTPKFLNP	DR	InterPro; IPR003521; IRR_typ.
Db	301 ETLKGKVKIEHTIKRKFVLFPSQTLKRYRVFSDMNIRMILTIADTHFTHMLCPQVPSTFNFLNF	DR	InterPro; IPR000157; TIR.
Qy	361 TQNVFTSIFEKSTLVKLTILQLQNGSLDKFLXGJLMPKPEYLNLYNTIESIRBDFTY	DR	Pfam; PF00475; IRR_1; 7.
Db	361 TQNVFTSIFEKSTLVKLTILQLQNGSLDKFLXGJLMPKPEYLNLYNTIESIRBDFTY	DR	Pfam; PF00560; IRR_1; 7.
Qy	421 KENCTWESIVVNLSSNMLTDVSFRCPPRIKUDLHSNKIKSVPKQVKLAEQLEAV	DR	Pfam; PF01463; IRRCT; 1.
Db	421 GENCTWESIVVNLSSNMLTDVSFRCPPRIKUDLHSNKIKSVPKQVKLAEQLEAV	DR	Pfam; PF01582; TIR_1.
Qy	481 AFNSTLDPGCGSFSSVSLTIDHSVSHPSADFFPSQCMRSIKAGDNPFQCTELRBF	DR	PRINTS; PR01537; INTRLKN1RF.
Db	481 ASNSLAHLPGCGSFSSSILSIDINSNSPASDFQSCOKIRSILKAGNNPFQCTELRDF	DR	PRINTS; PR00019; LEURICHRPT.
Qy	541 VKNIDQVSSEVLFQWPSYKCDPESYGSPLKDFHMSLSCNITLVTIGATMLVIAV	DR	SMART; SMO0082; LRRCT; 1.
Db	541 VKNIDQVSSEVLFQWPSYKCDPESYGSPLKDFHMSLSCNITLVTIGATMLVIAV	DR	SMART; SMO025; TIR_1.
Qy	541 IOLSGQVSSDVVPSWPDPSYCEPEPSYKGTLKDFRVSBLSCNTALLTIVTGVLAL	DR	PROSITE; PS00104; TIR_1.
Db	601 TWTSLCLYLDLPLWLRMVCQWTQTRRARNPBLELORNLOHAFAISSEHDSAWKKEI	DR	KW_Receptor.
Qy	601 TWTSLCLYLDLPLWLRMVCQWTQTRRARNPBLELORNLOHAFAISSEHDSAWKKEI	DR	SEQUENCE 793 AA; 90927 MW; C11C26009FB83668 CRC64;
Db	601 TWTSLCLYLDLPLWLRMVCQWTQTRRARNPBLELORNLOHAFAISSEHDSAWKKEI	DR	Best Local Similarity 79.5%; Score 3315; DB 2; Length 793; Matches 625; Conservative 73; Mismatches 86; Indels 2; Gaps 2;
Qy	661 VRYPLEKEDIQICLHERNRFVPGKSTVENINTCIEKSYKSIFVLSPNFVQSEWCHVLYFAH	DR	1 MIKOKESPTRCSHRTVYIVALVEGTIOPSDSEFSEWDMKTSIHLVPKLPKTKVLDLS
Db	661 VPCLEKEGKICLHERNRFVPGKSTVENINTCIEKSYKSIFVLSPNFVQSEWCHVLYFAH	DR	61 QNYTAELQVSDMSLSELTIVLRLSHNRQIQLDLSVFKENQDLEVILDSHNLQOKISCHPI
Qy	721 RHLFHESNNLILLEIPONSPINKKHKLAKMTORYLQPKPEKSKRGLWANTRA	DR	121 TTTLKHDLSFNDPDLAPICKERFENLTSOLNPLGLSAMKLUQDLIPTIAHLSYTLDLR
Db	721 RHLFHESNNLILLEIPONSPINKKHKLAKMTORYLQPKPEKSKRGLWANTRA	DR	180 NYIKENETESLQINAKTILVLFHPTSLFAIQNISVNTLGCLQLTNLKNDNCQVFI
Qy	781 FNMKLKLTVENNDVKS 796	DR	181 D-YMKENKKEKSLQINTKHLVPHPNFSVQFDISANSLGCLQLTNLKNDNCQVIL
Db	781 FNMKLKLTVENNDVKS 796	DR	240 KFSLBLUTRSTLLAFTNLHIEITWKLVLVRVQFLMPKPEYLNLYNTIESIRBDFTY
Qy	781 FNMKLKLTVENNDVKS 796	DR	240 KFSLBLUTRSTLLAFTNLHIEITWKLVLVRVQFLMPKPEYLNLYNTIESIRBDFTY
Db	300 SKTTKLALKTIEHTINQVLFPSQTLTYTVFSEMNIMLTSIDTPFTHMLCPHARSTPKFLN	DR	299 KFSLBLUTRSTLLAFTNLHIEITWKLVLVRVQFLMPKPEYLNLYNTIESIRBDFTY
Qy	300 YKTKLALKTIEHTINQVLFPSQTLTYTVFSEMNIMLTSIDTPFTHMLCPHARSTPKFLN	DR	300 SKTTKLALKTIEHTINQVLFPSQTLTYTVFSEMNIMLTSIDTPFTHMLCPHARSTPKFLN
Db	300 YKTKLALKTIEHTINQVLFPSQTLTYTVFSEMNIMLTSIDTPFTHMLCPHARSTPKFLN	DR	359 YKTKLALKTIEHTINQVLFPSQTLTYTVFSEMNIMLTSIDTPFTHMLCPHARSTPKFLN
Qy	360 FTQNVFTSIFEKSTLVKLTILQLQNGSLDKFLXGJLMPKPEYLNLYNTIESIRBDFTY	DR	360 FTQNVFTSIFEKSTLVKLTILQLQNGSLDKFLXGJLMPKPEYLNLYNTIESIRBDFTY
Db	360 FTQNVFTSIFEKSTLVKLTILQLQNGSLDKFLXGJLMPKPEYLNLYNTIESIRBDFTY	DR	360 FTQNVFTSIFEKSTLVKLTILQLQNGSLDKFLXGJLMPKPEYLNLYNTIESIRBDFTY
Qy	420 HKENCTWESIVVNLSSNMLTDVSFRCPPRIKUDLHSNKIKSVPKQVKLAEQLEAV	DR	420 HKENCTWESIVVNLSSNMLTDVSFRCPPRIKUDLHSNKIKSVPKQVKLAEQLEAV
Db	420 HKENCTWESIVVNLSSNMLTDVSFRCPPRIKUDLHSNKIKSVPKQVKLAEQLEAV	DR	420 HKENCTWESIVVNLSSNMLTDVSFRCPPRIKUDLHSNKIKSVPKQVKLAEQLEAV
Qy	480 VAFNSLTDLPGCGSFSSLVSLTIDHSVSHPSADFFPSQCMRSIKAGDNPFQCTELRE	DR	480 VAFNSLTDLPGCGSFSSLVSLTIDHSVSHPSADFFPSQCMRSIKAGDNPFQCTELRE
Db	480 VAFNSLTDLPGCGSFSSLVSLTIDHSVSHPSADFFPSQCMRSIKAGDNPFQCTELRE	DR	480 VAFNSLTDLPGCGSFSSLVSLTIDHSVSHPSADFFPSQCMRSIKAGDNPFQCTELRE
Qy	480 LASNSLAHLPGCGIFSSSILLENNSNSPASDFQSCOKIRSILKAGNNPFQSCELRD	DR	480 LASNSLAHLPGCGIFSSSILLENNSNSPASDFQSCOKIRSILKAGNNPFQSCELRD
Db	480 LASNSLAHLPGCGIFSSSILLENNSNSPASDFQSCOKIRSILKAGNNPFQSCELRD	DR	480 LASNSLAHLPGCGIFSSSILLENNSNSPASDFQSCOKIRSILKAGNNPFQSCELRD
Qy	540 FVKNIDQVSSEVLFQWPSYKCDPESYGSPLKDFHMSLSCNITLVTIGATMLVIA	DR	540 FVKNIDQVSSEVLFQWPSYKCDPESYGSPLKDFHMSLSCNITLVTIGATMLVIA
Db	540 FVKNIDQVSSEVLFQWPSYKCDPESYGSPLKDFHMSLSCNITLVTIGATMLVIA	DR	540 FVKNIDQVSSEVLFQWPSYKCDPESYGSPLKDFHMSLSCNITLVTIGATMLVIA
Qy	600 VWTSLCLYLDLPLWLRMVCQWTQTRRARNPBLELORNLOHAFAISSEHDSAWKSE	DR	600 VWTSLCLYLDLPLWLRMVCQWTQTRRARNPBLELORNLOHAFAISSEHDSAWKSE
Db	600 VWTSLCLYLDLPLWLRMVCQWTQTRRARNPBLELORNLOHAFAISSEHDSAWKSE	DR	600 VWTSLCLYLDLPLWLRMVCQWTQTRRARNPBLELORNLOHAFAISSEHDSAWKSE
Qy	660 LVVPLKEKEDIQICLHERNRFVPGKSTVENINTCIEKSYKSIFVLSPNFVQSEWCHVLYFA	DR	660 LVVPLKEKEDIQICLHERNRFVPGKSTVENINTCIEKSYKSIFVLSPNFVQSEWCHVLYFA
Db	660 LVVPLKEKEDIQICLHERNRFVPGKSTVENINTCIEKSYKSIFVLSPNFVQSEWCHVLYFA	DR	660 LVVPLKEKEDIQICLHERNRFVPGKSTVENINTCIEKSYKSIFVLSPNFVQSEWCHVLYFA

Qy	720	HENLFHEGSNNLILILEPPIRONSINKYKUKALMORTYLOWPKRSKRGCFWANTRA	779	Db	121	TTLKHLDLSFNFDDALPICKEGFLTQLNFGLGSATKQQLDLP1AHLHSCILDE	180
Db	720	HENLFHEGSNNLILILEPPIRONSINKYKUKALMORTYLOWPKRSKRGCFWANTRA	779	Qy	180	NYTYKEENETESENQILNKTTLHEVHPSPSLAQVNISVNTLGCLQNTNIKUNDNGCQVFI	239
Qy	780	AENMKL	785	Db	181	D-YMKENKKESLQLQINNTKKLHVHPNSPSVQVNDGNSLACQNLNKUNDNGCQVLL	239
Db	780	SINIKL	785	Qy	240	KELSELUTRGSTLNFTNHAETTWKCVLRVQFPLWAKPVEUNIYNTIESIREDPFTY	299
De				Db	240	KELSLGUGGPTLNFNTNHVETTWKCVLRVQFPLWAKPVEUNIYNTIESIREDPFTY	299
GN				Qy	300	SKTTLKALTIEHTNOVFLFSOTALYVFSENNIMMITISDTPFIRMLCPHAPSTPFLN	359
OS				Db	300	YKTTKLAKIENHTNKVIFFSOTALYVFSENNIMMITISDTPFIRMLCPHAPSTPFLN	359
AC	070602;	BOVIN	PRELIMINARY;	PRT;	793	AA.	
DT	05-JUL-2004,	integrated into UniProtKB/T+EMBL.					
DT	05-JUL-2004,	sequence version 1.					
DT	07-FEB-2005,	entry version 12.					
DE		Toll-like receptor 6.					
Name=tlr6;							
Bos taurus (Bovine).							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;							
Pecora; Bovidae; Bovinae; Bos.							
OX							
NCBI_TaxId=9913;							
RN	[1]						
RP							
RC							
RA							
RL							
RN	[2]						
NUCLEOTIDE SEQUENCE.							
RT							
Werling D.,							
Role of bovine TLRs in antigen response;"							
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.							
CC							
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distributed under the Creative Commons Attribution-NoDerivs license							
CC							
EMBL: AJ618974; CAF2015_1; -; mRNA.							
DR							
IMBL: AJ497803; AAY0896_1; -; mRNA.							
DR							
Ensembl: ENSBTAG0000014031; Bos taurus.							
DR							
GO: GO:0016020; C:membrane; IEA.							
InterPro: IPR00475; ILL_rcpt_1.							
DR							
InterPro: IPR00483; IRR_C.							
DR							
InterPro: IPR003591; LRR_Typ.							
DR							
PFam: PF00566; LRR_1; 7.							
DR							
PFam: PF04643; LRRCT_1.							
DR							
PRINTS: PR01537; INVRKNA1F.							
DR							
PRINTS: PR00019; LEVRICHRT.							
DR							
SMART: SMM0082; LRRCT_1.							
DR							
SMART: SMM0255; TIR_1.							
DR							
PROSITE: PSS0104; TIR_1.							
DR							
SEQUENCE	793	AA;	90927 MW;	D52422389B09F28F CRC64;			
Query Match							
Best Local Similarity	79.4%	; Score 3306;	DB 2;	Length 793;			
Matches	624;	Conservative	73;	Mismatches 87;	Indels 2;	Gaps 2;	
OS							
OC							
Mammalia; Eutheria; Burchontoglires; Gires; Rodentia; Sciurognathi;							
OC							
Muridae; Murinae; Murina; Rattus.							
OK							
NCBI_TaxId=10116;							
RN	[1]						
RP							
RC							
TISSUE=Pestette.							
DR							
MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;							
RX							
Strasbourg R.D., Collins F.S., Wagner L., Shearer C.M., Schuler G.D.,							
Klauser R.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhattacharya P.,							
Hopkins R.P., Jordon H., Moore T., Max S.I., Wang J., Hsieh F.,							
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,							
Stapleton M., Soares M.B., McDonald M.F., Carlson T.L., Scheetz T.E.,							
Brownstein M.J., Usdin T.B., Toshimori S., Carninci P., Prange C.,							
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,							

RA Bosak S.A., McBewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalon D.K., Muzny D.M., Soederberg N., Lu X., Gibbs R.A., Lu Y., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.B.,
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A., Bouffard G.G.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]
 RN RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Prostate;
 RA Director NCC Project;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DDJB databases.
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 DR EMBL; BCO62390; AAH2390.1; -; mRNA.
 DR SMR; Q6PQ90; 641-796.
 DR Ensemble; ENSRNOG0000000002161; Rattus norvegicus.
 GO; GO:0016020; C:membrane; IBA.
 GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR00475; ILL_rcpt_1.
 DR InterPro; IPR001611; LRR_C.
 DR InterPro; IPR000483; LRR_C.
 DR InterPro; IPR003591; LRR_TYP.
 DR Inter-Pro; IPR000157; TIR.
 DR Pfam; PF00560; LRR_1; 8.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO1537; INTFLKNR1P.
 DR SMART; SMO0369; LRR_TYP; 1.
 DR SMART; SMO0082; LRRCT; 1.
 DR SMART; SMO0255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR KW RECEPTOR. 806 AA; 92567 MW; F157F9D647DAF3A CRG64;
 SQ Query Match 75.8%; Score 3147.5; DB 2; Length 806;
 Best Local Similarity 74.2%; Pred. No. 3.6e-188;
 Matches 591; Conservative 91; Mismatches 113; Indels 1; Gaps 1;

QY 1 MTKDKDPIVKVSKFHVFVCLMIVTGVTRIQFSDSNEFAVDKSKQGLIHHPKDPLDKTVLDMS 60
 12 NSQDRPPIVESPHFVCTIALIVGSMWQPSDLSLESVUDYSNKNLTHPKDPLSPSTSLSLS 71
 QY 61 ONYIABLOVSMSPFSLBLTIRVLRSHRIOLDLDSVRLKPNQLEYLDSHNGNOKSCHPI 120
 72 QMSISDQLMSDLSFSLBLVRVLRSHRIIRRLDGFVFLNRRLDGVFLDVSQHNLQNTSCCPM 131

Db 121 VSFRLHDLSPFDKPAKIPCKFGNLSQLNFIQGLSAMKLQKDLPLTAHLHSYILDRN 180
 132 VNLKHLDSFNDPEVFLPVYKVRGFLNRLKLSFPLGISAKFRODLPLPISHLHSVLDLN 191

QY 181 YYIKENETESQIQLNAKTLHVFHPTSLFLAFQVNISVNTLGQLQTNKINDDNQCVFK 240
 192 YQIKDGTTESTQVNPNTVLHUVFHPNSLFQVNISTNALGQLOSNIKUNDENCOSLII 251

Db 241 FLSLELTFRGTSFLNFTLHETTWKCLVRFQFLPKVEVYNTLYNTIESIREEFTYS 300
 252 FLSLELTFRGTPFLNFTLHETTWKCFVRLFLWPMVEVYNTLYNTIESIREEFTYS 311

QY 301 KPTKALTIETHTNQVLFQSTALYTFSSENMIMMITISDPPIFLCPhAPSTKEFLNF 360
 312 EFLVLSLKIETHTNQVLFQFLVDAVLYSAFEMIRMLTISDTPFLHVCPEPFSTFLNF 371

QY 361 TQNFVFDISFFEKSTLVKLETLIQLQNLKDFKVGLMTKOMPSLEILDVSVNSLESGRH 420

Db 372 TQNVFTDTSIPOGCSTIKRLTTLIQLRGKLNFLKVALMTKMSLETLSVLSNLSNHVV 431

QY 421 KENCTWVESTVVLNLSSNMLMTDSVFRCLPPLPRIKVLDHSNIKKSVPQVKLEALQBLNV 480
 432 DRTCAWAESIRVLNLSNVNLSDSVFRCLPPLPKVLDHNRRVISPKDVTHLQLQELNV 491

Db 481 AFNSLTDLPCGGSSSLSVLIIDNSVSPRSADFFQSCKOVSRIKAGDAPFOCTCELREF 540
 492 ASNFLTDLPGCGAFSSLSVLVIDHNSVSHPSDDFFQSCONIRSTRAGNNPFRCTCELREF 551

QY 541 VKNIDQVSSLEGPDSYKCDPYSYRGSPLKDTHMSELSNCNTLIVTIGATMLVAV 600

Db 552 VKNIGQASREVSEGWPDSYKCDPYSIKGSPLODFHMSPLSCDTILTWTIGATLLAA 611

QY 601 TVTSICITYLDLPLWYIARMCOWTQTRRARNPYLELQRNQPHAFISYEHDSSAWVSEL 660

Db 612 IGASCLGYFLDPLWYIARMLMQWTQTRRARNPYLELQRNQPHAFISYEHDSSAWVSEL 671

QY 661 UPYLEKEDIOICLHERNFWGKSVTENVINCIEKSYKSVTRLSPWYFVQSEWCHBLYFAH 720

Db 672 LPNLEKDDIRVCLHERNFWGKSVTENVIIHIFIEXYSKISIFVLSPHFIQSEWCHBLYFAH 731

QY 721 HNLFHGSSNNLILLEPIONSTINKYKULKALMORTVLIQWPKESKRGFLMANRA 780

Db 732 HNLFHGSSNNLILLEPIQCNNTISRYHKURALMAQRTYLEWPIEKGKRGFLWANLRA 791

QY 781 FNMKLTIVTENNDVKS 796

Db 792 FIMKLALVNE-NDVKT 806

GN Name-Tlr6;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorpha;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA].

RC TISSUE=Embryo;

RX MEDLINE=99250250; PubMed=10231569; DOI=10.1073/pnas.250476497;

RA Takeuchi O., Kawai T., Copeland N.G., Gilbert D.J., Jenkins N.A., Takeda K., Akira S.;
 RT "Tlr6: a novel member of an expanding Toll-like receptor family." Gene 231:59-65 (1999).

RN [2]

RP NUCLEOTIDE SEQUENCE [mRNA], AND MUTAGENESIS OF PRO-680.

RC STRAIN=BALB/C; TISSUE=Macrophage;

RC MEDLINE=20558531; PubMed=11095740; DOI=10.1073/pnas.250476497;

RA Ozinsky A., Underhill D.M., Fontenot J.D., Hajjar A.M., Smith K.D., Wilson C.B., Schroeder L., Ademre A.;
 RT "The repertoire for pattern recognition of pathogens by the innate immune system is defined by cooperation between Toll-like receptors." Proc. Natl. Acad. Sci. U.S.A. 97:13766-13771 (2000).

CC -!- FUNCTION: Participates in the innate immune response to Gram-positive bacteria and fungi. Acts via MyD88 and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response. Cooperates with TLR2 for the cellular activation (By similarity).

CC -!- TISSUE SPECIFICITY: Detected in thymus, spleen, ovary and lung.

CC -!- SIMILARITY: Belongs to the toll-like receptor family.

-!- SIMILARITY: Contains 14 LRR (leucine-rich) repeats.
 -!- SIMILARITY: Contains 1 TIR domain.

CC EMBL; AB020808; BRAV632_1; ALT_INIT; mRNA.
 CC EMBL; AF314636; AAG18563_1; ALT_INIT; mRNA.
 CC HSSP; O15399; 1FYV.
 CC SMR; O9EP99; 630-785.
 CC Ensemble; ENSMUSG0000051498; Mus musculus.

DR MGI; MGI:1341296; TIR6.
 GO; GO:0016021; C:integral to membrane; TAS.
 GO; GO:0016020; C:membrane; ISS.
 DR GO; GO:005335; C:phagocytic vesicle; ISS.
 DR GO; GO:008034; F:lipoprotein binding; IMP.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007246; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:002116; P:macrophage activation; ISS.
 DR GO; GO:005084; P:positive regulation of interleukin-12 biosyn.; ; NAS.
 DR GO; GO:005410; P:positive regulation of interleukin-6 biosyn.; ; ISS.
 DR GO; GO:0042088; P:T helper 1 type immune response; IC.
 DR InterPro; IPR004075; ILL_rcpt_1.
 DR InterPro; IPR01611; LRR.
 DR InterPro; IPR000483; LRR_C.
 DR InterPro; IPR003591; LRR_typ.
 DR SMART; SMM0369; LRR_TYP; 1.
 DR SMART; SMM0082; LRR_C; 1.
 DR SMART; SMM0255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Glycoprotein; Immune response; Innate immunity;
 KW Leucine-rich repeat; Membrane; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 195 Toll-like receptor 6.
 /FTID-PRO_000004732.
 FT TOPO_DOM 28 584 Extracellular (Potential).
 FT TRANSMEM 585 605 Potential.
 FT TOPO_DOM 606 795 Cytoplasmic (Potential).
 FT REPEAT 32 51 LRR 1.
 FT REPEAT 52 75 LRR 2.
 FT REPEAT 76 98 LRR 3.
 FT REPEAT 100 120 LRR 4.
 FT REPEAT 121 144 LRR 5.
 FT REPEAT 146 171 LRR 6.
 FT REPEAT 225 248 LRR 7.
 FT REPEAT 330 353 LRR 8.
 FT REPEAT 376 399 LRR 9.
 FT REPEAT 402 425 LRR 10.
 FT REPEAT 427 449 LRR 11.
 FT REPEAT 459 472 LRR 12.
 FT REPEAT 473 496 LRR 13.
 FT REPEAT 498 517 LRR 14.
 FT DOMAIN 640 784 TIR.
 FT CARBOHYD 42 42 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 114 114 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 144 144 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 195 195 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 214 214 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 253 253 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 285 285 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 359 359 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 401 401 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 434 434 N-linked (GlcNAc. .) (Potential).
 FT MUTAGEN 680 680 p->H: Dominant negative mutant, blocks response to Gram-positive pathogens.

FT	CONFLICT	181	181	Y -> H (in Ref. 1)
SEQUENCE	795 AA;	9116 MW;	34DBD17SA26C233	CRC64;
Query Match		75.7%	Score 3144.5;	DB 1;
Best Local Similarity		73.9%	Length 795;	
Matches	588;	Conservative	Pred. No. 5.4e-18;	
Matches	588;	Conservative	Mismatches 110;	Indels 1;
Matches	588;	Conservative	Gaps 1;	
Qy	1 MTKDKEDIVKSFHFCVCLMILIVGTRIQFSDGNEFAVDKSKGRLHVPRDPLIKTVDMS	60		
Db	1 MSQDRKFKIVGSHFHVCALIALVGSMPPFSNELESMDYNSRNALTHYPPDKLPRTKALSL	60		
Qy	61 QNYIAELQVSIMNFSLSLTIVLSHARIQLQDLSVFENQDOLYELDSHNOLOKISCHPI	120		
Db	121 VSFRHDLISFNDPKALICKERFGNLSQLNFIGLSAMKQKQDILPAWHLHSYIUDLN	180		
Qy	181 YYIKKENETESTQINAKTLYLHFPTSLFATQVNISNTGCOLTNIKLNDNCQFIK	240		
Db	181 YHKGGETESLOIPNPTVYLHVPHNPNSLSQVNMSVNALGHQLSNIKLNDNCQFIK	240		
Qy	241 FISELTGTSFLNFTLHETTWKCIJVRFOFLWPKEVEINYNTITIEIREEFTYS	300		
Db	241 FISEBLTGTGPTLNUVTQHETTWKCSVLKFQFWPRAVEVLYNLTITERDREFTYS	300		
Qy	301 KITLKALTAIEHTINQVQLFSQTALTYVSEANIMMITISDPPRIMCPHAPSTKEFLNF	360		
Db	301 ETALKSMLERVKNOFLPSKEALVSEAEIMKMSISDPFPHMCPSPSSFTLFN	360		
Qy	421 KENCTWIVTUNLNSNMILDSVFRCLPPLKVLHNRMSIPDVTHLQALQBILN	480		
Db	421 DRTCAWAEKSLVLUVLSSNMLTSVFRCLPPLKVLHNRMSIPDVTHLQALQBILN	480		
Qy	481 AFNSLTDLPGGFSSSLVLDHNSVSHPADFPCQOKRSIKADDNPQCTCEREP	540		
Db	481 ASNLSLDPGGCAFSSSLVLDHNSVSHPADFPCQOKRSIKADDNPQCTCEREP	540		
Qy	541 VKNIDQSVSELEGWPDSYKCDYPS3YGRSPKLDFINSESCNITLAVLIVTGA	600		
Db	541 VKNIGWVAREVEGWFDSYKCDYPS3KGTALDFINPLSPCDTVLITVIGATMVLAV	600		
Qy	601 TVTSCLCYLDAPWLYRNVCQWTRARRNPLPELQRNQPHAFYSSYESEIDSAWTKSEL	660		
Db	601 TGAFLCILYFDLWVYWRMLCQWTOHRHARHPLLEFLQRNQPHAFYSSYESEIDSAWTKSEL	660		
Qy	661 VYPLEREDIQICLHERNFVPGKSIVENIINCIEKSYISFLVSPNWTQSENCHELYFAH	720		
Db	661 LPNLEKDDIDYVCLHERNFVPGKSIVENIINCIEKSYISFLVSPNWTQSENCHELYFAH	720		
Qy	721 HNLFHEGGSNNLTLLEPIPONISPINKYKUKALMTQRTYQWPKEKSKGFLWANIRAA	780		
Db	721 HNLFHEGGSNNLTLLEPILQONNIPSYRKURALMAORTYLEMPTEKGKGFLWANIRAS	780		
Qy	781 FNKLKLVTTENNDVKS 796			
Db	781 FIMKLAIVNE-DDVKT 795			
RESULT	8			
ID	Q3UV88_MOUSE			
AC	O3UV88;			
DT	11-OCT-2005, integrated into UniProtKB/TREMBL.			
DT	11-OCT-2005, sequence version 1.			
DT	07-FEB-2005, entry version 5.			
DE	Adult male bone cDNA, RIKEN full-length enriched library, clone:9830120H05 product:toll-like receptor 6, full insert sequence.			

- GN Name=Tl6;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteraria; Euarchontoglires; Gires; Rodentia; Sciurognathi;
 OC Murioidea; Muridae; Murinae; Mus.
 NCBI_TAXID=10090;
 RN [1] _TAXID=10090;
 RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning.;"
 RT Methods Enzymol. 303:19-44 (1999).
 RL Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima P., Furuno M., Futaki S., Garibaldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummicki L., Iacono A., Ishikawa T.,
 RA Jakt M., Kanapin A., Karch M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Koilias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Larneau I.F., Lazarus G., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuza S., Mikl H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishioka S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavani W.J., Pavesi G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shiba T., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugimura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegnér J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamamoto H., Zabarcosky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmel M.S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niinomiya N.,
 RA Nishio T., Okeda M., Plesey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.; "The transcriptional landscape of the mammalian genome.;"
 RL Science 309:1559-1563 (2005).
 RN [2] _TAXID=10090;
 RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX PubMed=1641073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.;"
 RL Science 309:1564-1566 (2005).
 RN [3] _TAXID=10090;
 RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furukawa M., Kasukawa T., Adachi J., Itoh M., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamakawa T., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nagami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Schackenbach J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Drabani T., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Garibaldi M., Giros C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konigaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltzis L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavani W.J., Pertea G., Pesole G.,
 RA Petrusky N., Pilai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Sehou M., Shimada K.,
 RA Sultan A., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo J., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yangaisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu H., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraishi T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki K., Shinohara M., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RT Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of full-length cDNAs.;"
 RT Nature 420:563-573 (2002).
 RN [4] _TAXID=10090;
 RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa H., Shibusawa K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kyoyama H., Kondo S., Yamamoto I.,
 RA Saito T., Okada K., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaiko I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barth G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shihata Y.,
 RA Suzuki H., Toyokuoka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.;"
 RT Nature 405:685-690 (2000).
 RN [5] _TAXID=10090;
 RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=2049934; PubMed=1102159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata K., Saito R., Suzuki H., Tomaru Y.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.;"
 RT Genome Res. 10:1617-1630 (2000).
 RL Genome Res. 10:1617-1630 (2000).
 RN [6] _TAXID=10090;
 RP NUCLEOTIDE SEQUENCE;
 RC STRAIN=C57BL/6J; TISSUE=Bone;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aiawa M., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitisuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishime H., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RA "RIKEN integrated sequence analysis (RSA) system-384 format sequencing pipeline with 384 multicapillary sequencer.;"
 RT Genome Res. 10:1757-1771 (2000).
 RN [8] _TAXID=10090;

RA	STRAINC57BL/6J; TISSUE:Bone;	QY	541 VKLIDQVSEVILFGMPDSYKCPESYRGSPKDFHMSSELSONNITIIVTGMIAV 6000
Hori F., Iida J., Imamura K., Inotani K., Itoh M., Kanagawa S., Kawai J., Koijima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Takami M., Tagami Y., Waki K., Watanuki A., Muramatsu M., Hayashizaki Y.	R.A. Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.	RA	552 VKNQGWWAREVVGWPSYRCYDPESSKGTAARDFHMSPLSCOTVLLVITGATMLVIAV 6111
RA	GO; GO:0016020; C:membrane; RCA.	QY	601 TVTSCLCYLDLPPWLRMWCQWTOTRRARNPPIEELORNLOQHAFISSEBHSAWVSEL 6600
CC	GO; GO:000488; P:transmembrane receptor activity; RCA.	CC	612 TGAFLCYFDLRYVURMCQWTOTRHARHIEELORNLOQHAFISSEBHSAWVSEL 6711
DR	EMLB; AK137502; BAE23384.1; -; mRNA.	DR	612 TGAFLCYFDLRYVURMCQWTOTRHARHIEELORNLOQHAFISSEBHSAWVSEL 6711
DR	MGI; MGI-141296; TIR.	DR	612 TGAFLCYFDLRYVURMCQWTOTRHARHIEELORNLOQHAFISSEBHSAWVSEL 6711
DR	GO; GO:0016021; C:integral to membrane; RCA.	QY	661 VPLTEKEPDIOICLHERNFVPGKSVIENINCTEKSYSFIVSPNPFYQSEWCHYLFH 7200
DR	Pfam; PF00590; LRR_1; 6.	DR	672 LPNLXEDDIRVCLHERNFVPGKSVIENINCTEKSYSFIVSPNPFYQSEWCHYLFH 7311
DR	Pfam; PF0163; LRRCT; 1.	DR	721 HNFHEGSNLLILLEPIRQNSIPNPKHKLALMPTQYQPKERSKGLFWANRAA 7800
DR	PRINTS; PRO1537; INTRAKRNAP.	DR	732 HNFHEGSNLLILLEPIRQNSIPNPKHKLALMPTQYQPKERSKGLFWANRAA 7911
DR	SMART; SM00369; LRR_TPR; 1.	DR	781 FNKKLTLYTENDVKS 796
DR	SMART; SM00082; LRRCT; 1.	DR	792 PIMKLALVNE-DDVKT 806
DR	PROSITE; SM00255; TIR; 1.	DR	
KW	Receptor.	DR	
SEQUENCE	806 AA; 92394 MW; 6FD0CD4CB8FA5741 CRC64;	DR	
Query Match	75.7%; Score 3144.5; DB 2; Length 806;	DR	
Best Local Similarity	73.9%; Pred No. 5.5e-188;	DR	
Matches	588; Conservative 97; Mismatches 110; Indels 1; Gaps 1;	DR	
1	MTKDEKEPTVKPSFHFCVUMLVINGTRIQFSDGNEFAVDKSKRGLIHVKPDLPLKTKVLMS 60	DR	
12	MSQDRKPKIVGFSFHFCVACALIVGSMTPFSNEELSMWVDSNRNLTHVPKDLPPTKALIS 71	DR	
61	QNTIAELQVSDMSFLLSEITVLRUSHNRQLQDDLSVFKENQDLEYLIDLISHNQLQKISCHPI 120	DR	
72	QNSISLERMPDIFSELRVLRUSHNRQLRSLDPHFLFNQDLEYLIDLISHNRLQKISCPM 131	DR	
121	VFRHDLISFNDKALPKICKERFLNLSQFLGSAKMKLQKDLIPTAHLSTYLQDURN 180	DR	
132	ASIRHLDSLFDNDLPIVCKEFGNLKTFPLGLSAKERFQDLDLIPVAMHLSCILDLVS 191	DR	
181	YKVKENETESLQLINKAKLHLVPHPTSLRAIQNISVTLGCLQLTNIKLNDDNCQPIK 240	DR	
192	YHKGGETESLQLQPNTVHLVPHPNLFSVQNMWSVALGHQOLSNKLNBNQCRMLT 251	DR	
241	FSELBLTRGSTLNFTLNHETTWWKCLVRFQFLWPKPVPEYLNNTNTLTIESTREDFMYS 300	DR	
252	FUSELTTRGPTLLANTLQHETTWKCSVKLPOFFWPRPEYLNLYNLTTERIDREFTYS 311	DR	
301	KTKLKLALTEHTINOQEVFSQTYVESEMNTIMMLTSDTPTHMCPHAASSTKFELNF 360	DR	
312	ETALKLSEMEHVKQVUFPSKESKALYVSAEMNTKMLSISDTPTHMCPHSSTKFELNF 371	DR	
361	TQNVFTSISPEKCSLTVKSLVQKLTQIQLKQGLKDFKVGMLTKDMPSLEJLDVMSLSEGRH 420	DR	
372	TQNVFTSISVFOGSTKRLQTLQLRQNGKLFKVAINTKOMSLETDLUSLNSHAY 431	DR	
421	KENCTWTSIVVNNLSNNMLTDSVFRCLPPIRKVTDLHSNKRSVPKPKVVKLAQELNV 480	DR	
432	DRTCAWAESILVNLNSNNMLTGSVFRCLPPIRKVTDLHSNKRSVPKPKVVKLAQELNV 491	DR	
481	AFLSTDPDGCGESPSLSVLTDHNSVSHPSADPFOSSOKMSIKAGDNFOCTCEUREF 540	DR	
492	ASISLTDLGCGAFSSISVLTDHNSVSHPSADPFOSSOKMSIKAGDNFOCTCEUREF 551	DR	
DR	SIRK; QTPC5; 641-796.	DR	
Ensembl; ENSMUSG0000051498; Mus musculus.	Ensembl; ENSMUSG0000051498; Mus musculus.	DR	
QY	NUCLEOTIDE SEQUENCE.	RP	
RA	STRAIN-C3H/He; TISSUE:Osteoblast;	RA	
RA	Strain-Berg R.; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.	RA	
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	CC	
CC	Distributed under the Creative Commons Attribution-NoDerivs License	CC	
DR	EMLB; BC053366; AAH55366.1; -; mRNA.	DR	
DR	HESP; QTPC5; 1FVY.	DR	
DR	Ensembl; ENSMUSG0000051498; Mus musculus.	DR	

DR MGI; MGI:1341296; TIR6.
 DR GO; GO:0016021; C:integral to membrane; RCA.
 DR GO; GO:0016020; C:membrane; RCA.
 DR GO; GO:004887; F:transmembrane receptor activity; RCA.
 DR InterPro; IPR04075; ILL_rcpt_1.
 DR InterPro; IPR01611; LRR_C.
 DR InterPro; IPR00483; LRR_C.
 DR InterPro; IPR003591; LRR_TYP.
 DR Pfam; PF01560; LRR_1; 6.
 DR Pfam; PF01463; LRR_C; 1.
 DR SMART; SM00369; LRR_TYP; 1.
 DR SMART; SM0002; IRR_C; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Receptor.
 SEQUENCE 806 AA; 92408 MW; 24830B28BB3C3546 CRC64;

Query Match 75.7%; Score 3143.5; DB 2; Length 806;
 Best Local Similarity 73.7%; Pred. No. 6.4e-188; Matches 587; Conservative 98; Mismatches 110; Indels 1; Gaps 1; RT
 QY 1 MTKDKEPIVKSFHFCVCLMILVGTRIQFSDNEFAVDKSKEGLIHVPKDIPLTKVLDMS 60
 Db 12 NSQSDRKRPIVGSFHFVCALALIVGSMWPSNLSMDSWYNSNLTHPKDIPPTKALIS 71
 QY 61 QNYTIALQLOVSMFSLSLTAVRLSHRIQLQDLSVFKPNDQLEYIDLISHNQLOKUSCHPI 120
 Db 72 QMSISELRMPDLSFLSELBRVLRVLRSHNRISLDPFHVLFLFNQDDELYDQVSNHLQNISCCPM 131
 QY 121 VSFHRHDLSFDIFPKALPICKFGNLSQLNPGFLSANKLQDKLPLTAHLHSYIILDLRN 180
 Db 132 ASIRHDLISFDIFPKALPICKFGNLSQLNPGFLSANKLQDKLPLTAHLHSYIILDLRN 191
 QY 181 YVIKENETESIQLINAKTLHVFHPTSLFATQWNISUNTLGQLOLTNIKENDDNCOVFIK 240
 Db 192 YHKGGETESTSQQIPNTVILHVPHPNLSFSQVNMSNALSHLQNSNKUNDENCPMT 251
 QY 241 FLSLELTGRGSTLNFNTLHETTWKCLYRVDFPLWPKREVEYNINYNTIESIREEFTYS 300
 Db 252 FLSLELTGRGSTLNFNTLHETTWKCLYRVDFPLWPKREVEYNINYNTIESIREEFTYS 311
 QY 301 KUTKLKALTIERTHNTQVLFQSQTALYTWFSEMMIMMUTSDPPFHMCYPHPAPSTEKFNP 360
 Db 312 FLSLELTGRGSTLNFNTLHETTWKCLYRVDFPLWPKREVEYNINYNTIESIREEFTYS 371
 QY 361 TONVFTDSIEFKCSTLVKLETLIQLQNGLKDIFKVGLMTKOMPSLETFDVSNSLSEGRH 420
 Db 372 TONVFTDSVFCQCSLRLQTLIQLQNGLKDIFKVGLMTKOMPSLETFDVSNSLSHAY 431
 QY 421 KENCTWAVESTIVTNLSSNMUDSVFRCIPLPRKVLDAHSNKTISKVPKQVWVLEALQBLYV 480
 Db 432 DRTCAWAESIVLVLNLSNMUTSVFRCIPLPRKVLDAHSNKTISKVPKQVWVLEALQBLYV 491
 QY 481 AFNSLTDLPGCGFSSLSVLDHNSSHPSADFFOSCQKRSIKAGDNPPQCTCEREP 540
 Db 492 ASNSTDLPGCGFSSLSVLDHNSSHPSADFFOSCQKRSIKAGDNPPQCTCEREP 551
 QY 541 VKNIDQSSSEVLEGWPDSYKCDPESYRGSPKDFHMSLBNITLIVTGATMULAV 600
 Db 552 VENIGWWAREVEWGWPDSYKCDPESYRGSPKDFHMSLBNITLIVTGATMULAV 611
 QY 601 TWTSLCIYLDDFLWYLRMWCQWOTRRAPIRANTPEELORNQHAFHTSYSEEDSAWTEL 660
 Db 612 TGAFLCLYFDLFWYRMWCQWOTRRAPIRANTPEELORNQHAFHTSYSEEDSAWTEL 671
 QY 661 VVYLEKDIQICLHERHFPVPGSIVVENTINCERKSYKSIIFVSPNPFQYQSEWCHYELYFAH 720
 Db 672 LNLNEKODDIRVCLHERHFPVPGSIVVENTINCERKSYKSIIFVSPNPFQYQSEWCHYELYFAH 731

RESULT 10
 TLR1_HUMAN ID_TLR1_HUMAN STANDARD; PRT; 786 AA.
 AC Q15399; O15452; Q09990;
 DT 31-JAN-2002, integrated into UniProtKB/Swiss-Prot.
 DT 31-JAN-2002, sequence version 2.
 DT 07-MAR-2006, entry version 57.
 DE Toll-like receptor 1 precursor (Toll/interleukin-1 receptor-like protein) (TIR) (CD281 antigen).
 DE Name=TLR1; Synonyms=KIAA0012;
 OS Homo sapiens (human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RC TISSUE=Erythroleukemia;
 RX MEDLINE=981856; PubMed=9435236; DOI=10.1073/pnas.95.2.588;
 RA Rock F.L., Hardiman G., Timans J.C., Kastlein R.A., Bazan J.F.;
 RT "A family of human receptors structurally related to Drosophila toll."
 RT Proc. Natl. Acad. Sci. U.S.A. 95:588-593 (1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
 RC TISSUE=Bone marrow; PubMed=7584026; DOI=10.1093/dnare/1.1.27;
 RX MEDLINE=96051387; PubMed=7584026;
 RA Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y.,
 RA Sato S., Nagase T., Seki N., Ishikawa K., Tabata S.;
 RT "Prediction of the coding sequences of unidentified human genes. I: The coding sequences of 40 new genes (KIAA0011-KIAA0050) deduced by RT analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1.";
 RT DNA Res. 1:27-35 (1994).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
 RC TISSUE=Brain;
 RX MEDLINE=21154917; PubMed=1120166; DOI=10.1101/gr.154701;
 RA Wiemann S., Weil B., Wellenreuther R., Gassnerhuber J., Glaesl S.,
 RA Ansorge W., Boecker M., Bloecker H., Bauerbach S., Blum H.,
 RA Lauber J., Duesterhoft A., Beyer A., Koehler K., Strack N.,
 RA Mewes H.-W., Ottewohlweiler B., Obermaier B., Tampe J., Heubner D.,
 RA Wambott R., Korn B., Klein M., Pousta B.A.;
 RT "Towards a catalog of human genes and proteins: sequencing and RT analysis of 500 novel complete protein coding human cDNAs.";
 RT Genome Res. 11:422-435 (2001).
 RN [4]
 RP PROTEIN SEQUENCE OF 25-39.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites";
 RT Protein Sci. 13:2819-2824 (2004).
 RN [5]
 X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF TIR DOMAIN.
 RX MEDLINE=2051768; PubMed=11031518; DOI=10.1038/s5040600;
 RA Xu Y., Tao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
 RT "Structural basis for signal transduction by the Toll/interleukin-1 receptor domains";
 RL Nature 408:111-115 (2000).
 CC - FUNCTION: Participates in the innate immune response to microbial agents. Cooperates with TIR2 and modulates the response to microbial constituents. Acts via MyD88 and TRAF6, leading to NF- kappa-B activation, cytokine secretion and the inflammatory

FT	VARIANT	118	118
CC	response (By similarity).		
-i- SBDUNIT: Binds TLR2 via their respective extracellular domains.			
CC	Bands MyD88 via their respective TIR domains (By similarity).		
-i- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and			
CC	phagosomes (By similarity).		
-i- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in spleen, ovary,			
CC	peripheral blood leukocytes, thymus and small intestine.		
-i- SIMILARITY: Belongs to the Toll-like receptor family.			
CC	-i- SIMILARITY: Contains 8 LRR (leucine-rich) repeats.		
CC	-i- SIMILARITY: Contains 1 TIR domain.		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the Creative Commons Attribution-NonDerivs License		
CC	EMBL; U88540; AAC34137.1; -; mRNA.		
DR	EMBL; D13637; BAA02801.2; ALT_INIT; mRNA.		
DR	EMLBL; AL050262; CAB43364.1; -; mRNA.		
DR	PIR; T08664; T08664.		
DR	PDB; 1PFV; X-ray; A=625-785.		
DR	Ensembl; ENSG00000174125; Homo sapiens.		
DR	H-INVDB; HIX004160; -.		
DR	HGNC; HGNC:11847; TLR1.		
DR	MIM; 601194; gene.		
DR	GO; GO:0045335; C:integral to plasma membrane; TAS.		
DR	GO; GO:0005887; P:phagocytic vesicle; ISS.		
DR	GO; GO:0048887; P:transmembrane receptor activity; NAS.		
DR	GO; GO:0042497; P:tricarboxylate transporter activity; ISS.		
DR	GO; GO:0042750; P:activation of NF-kappaB-inducing kinase; ISS.		
DR	GO; GO:0042495; P:detection of tricarboxylated bacterial lipoprotein; ISS.		
DR	GO; GO:0006555; P:immune response; TAS.		
DR	GO; GO:0042316; P:macrophage activation; NAS.		
DR	GO; GO:0045410; P:positive regulation of interleukin-6 biosynthesis; ISS.		
DR	GO; GO:0042535; P:positive regulation of tumor necrosis factor; ISS.		
DR	GO; GO:0007165; P:signal transduction; TAS.		
DR	InterPro; IPR004075; IIL_rcpt_1.		
DR	InterPro; IPR01611; LRR.		
DR	InterPro; IPR00483; LRR_C.		
DR	InterPro; IPR03591; LRR_TYP.		
DR	InterPro; IPR000157; TIR.		
DR	InterPro; IPR00157; TIR.		
DR	Pfam; PF0163; LRRCT_1.		
DR	Pfam; PF01582; TIR; 1.		
DR	PRINTS; PR01537; INTRAKNIRF.		
DR	PRINTS; PR00019; LEURICHRPT.		
DR	SMART; SM00082; LRRCT_1.		
DR	SMRTB; SM00255; TIR; 1.		
DR	PROSITE; PSS0104; TIR; 1.		
KW	immune response; inflammatory response; Tonate immunity;		
KW	leucine-rich repeat; Membrane; Polymorphism; Receptor; Repeat; Signal;		
FT	SIGNAL	1	24
FT	CHAIN	25	786
FT	Toll-like receptor 1.		
FT	/PRID=PRO 000003405.		
FT	Extracellular (Potential).		
FT	Potential.		
FT	Cytoplasmic (Potential).		
FT	LRR 1.		
FT	LRR 2.		
FT	LRR 3.		
FT	LRR 4.		
FT	LRR 5.		
FT	LRR 6.		
FT	LRR 7.		
FT	LRR 8.		
FT	DOMAIN	635	779
FT	CARBHYD	51	51
FT	CARBHYD	137	137
FT	CARBHYD	163	163
FT	CARBHYD	330	330
FT	CARBHYD	429	429
FT	CARBHYD	578	578
QY	Query Match	69.1%	Score 2830; DB 1; Length 786;
QY	Best Local Similarity	69.5%	Pred. No. 2.5e-168;
QY	Matches 540; Conservative	92;	Mismatches 143; Indels 2; Gaps 1;
Db	5 FHFHFAIFMILQIRIQIOLSEESERFLVDRSKNGLHLHVPKDQLPLKTVLDMSONTQALQSD	71	72 MFSFELSTVLRSHNRQLQDLSVKEFNQEDLEYLDLSHNOLOKISCHAVISFRHDSFN
QY	12 FHFHFAIFMILQIRIQIOLSEESERFLVDRSKNGLHLHVPKDQLPLKTVLDMSONTQALQSD	71	65 ILSISKURILISHNRQLQDLSVKEFNQEDLEYLDLSHNOLOKISCHAVISFRHDSFN
Db	5 FHFHFAIFMILQIRIQIOLSEESERFLVDRSKNGLHLHVPKDQLPLKTVLDMSONTQALQSD	64	72 MFSFELSTVLRSHNRQLQDLSVKEFNQEDLEYLDLSHNOLOKISCHAVISFRHDSFN
QY	132 DFKALPICKERGLNSQNLFLGSLAMKLUQDLPRIAHMLSLVILLDRNYYKENETSL	191	192 QLNAAKTHLVLFIHPTSLTAIQNISVNLTGCLQLTNIK-LIDDNQCVFKEFSLBUTRGS
Db	125 AF6ALPICKERGLNSQNLFLGSLAMKLUQDLPRIAHMLSLVILLDRNYYKENETSL	184	192 QLNAAKTHLVLFIHPTSLTAIQNISVNLTGCLQLTNIK-LIDDNQCVFKEFSLBUTRGS
QY	185 QDFNTESLHIVFFTKERFLQFLDKPSLQFLGUSTTHLEKSSTLPLIAHNISKYLVGETYERKEDPEGI	244	192 QLNAAKTHLVLFIHPTSLTAIQNISVNLTGCLQLTNIK-LIDDNQCVFKEFSLBUTRGS
Db	250 TLNFNTLHIIETWKCLYRVFLWLWPKVEVNNYNTIES:REEDDTYSKTYLALTI	309	192 QLNAAKTHLVLFIHPTSLTAIQNISVNLTGCLQLTNIK-LIDDNQCVFKEFSLBUTRGS
QY	245 KLSSTLNNIETTWNFSFIRLQDVWHTVWYISISNVKLQGQDFRDYDSESTSLKALSI	304	192 QLNAAKTHLVLFIHPTSLTAIQNISVNLTGCLQLTNIK-LIDDNQCVFKEFSLBUTRGS
Db	310 EHTINQVLFQSFQALYTWFSEMMNIMMLTISPRPFHMLCPHAPSPTFKELNFQVFTSI	369	192 QLNAAKTHLVLFIHPTSLTAIQNISVNLTGCLQLTNIK-LIDDNQCVFKEFSLBUTRGS
QY	: : : : : : : : : : : : : : : : : :	364	305 HQQVSDVGFQPOSIVYEFNSNMNKNFVSGTRMVLCPKLSKSPFLHDFSNMLLTDV
Db	370 FEKSTLVYKLETLILOKGLDKLFKGVLGMKOMPSLELDVSVMSLESGRHRHENCTWES	429	305 HQQVSDVGFQPOSIVYEFNSNMNKNFVSGTRMVLCPKLSKSPFLHDFSNMLLTDV

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 CC
 Db FENCGHILTELETLIQLQNLQNLKSLKAEMTQMKSLOQDLSQNSVYDEBKRGDCSWTKS 424
 QY 430 IWLNLSSNMITDSVRLPPIKVLQDHNSKIKSPKQVNLQELNVAFNSTLDP 489
 : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
 425 ILSLNMSNLTIDTFRCLPPRKLVKDHLNSKIKSPKQVNLQELNVAFNSTLDP 484
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:004888; F:transmembrane receptor activity; IEA.
 DR KW Receptor.
 SQ SEQUENCE 786 AA; 90290 MW; 1406C60FB5847F5B CRC64;
 QY 490 GCGSFSSLVILIDANSVHSADFFOSCOQRISKAGDNPFQCTCLREVNIDQVS 549
 485 GCGSFSSLVILIDANSVHSADFFOSCOQRISKAGDNPFQCTCLREVNIDQVS 544
 550 EVLEGEDPSYKDYPESYRGSPKLDFHMSETISCNITLIVTGTATMLVLAUTVSLCYL 609
 545 EVLEGEDPSYKDYPESYRGSPKLDFHMSETISCNITLIVTGTATMLVLAUTVSLCYL 604
 Db 610 DLPWYLRMVCWTQTRRARNIPLEBLORNQPHAFYHSYRDHSANKSELVPLYKEDEDI 669
 605 DLPWYLRMVCWTQTRRARNIPLEBLORNQPHAFYHSYRDHSANKSELVPLYKEDEDI 664
 QY 670 QICLHERNFVGKSVENINCIKSYKSIPLSPNPNQVOSWCHYLYFAHNLFHEGSN 729
 Db 665 QICLHERNFVGKSVENINCIKSYKSIPLSPNPNQVOSWCHYLYFAHNLFHEGSN 724
 QY 730 NLLILLEPIQONSPNKYHKLAKMORTLQWPKRSKGFLFWANRAINKLT 786
 Db 725 SLILLEPIQYSIPSSYHKLKSMLARRTLEWPKEKSKGLFWANRAINKLT 781
 RESULT 11
 032MK3 HUMAN PRELIMINARY; PRT; 786 AA.
 ID 032MK3 - HUMAN PRELIMINARY; PRT; 786 AA.
 AC 032MK3;
 DT 06-DEC-2005, integrated into UniProtKB/TREMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Toll-like receptor 1.
 GN Name=TLR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Krausmer R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 Altchul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Borodllo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin B., Toshiyuki S., Casarino P., Prange C.,
 Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Blakesley R.W., Toucman J.W., Green E.P., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Skalska M.T., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Bouffard G.G.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., Smailus D.B.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MGC Project;
 RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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 CC
 Db FENCGHILTELETLIQLQNLQNLKSLKAEMTQMKSLOQDLSQNSVYDEBKRGDCSWTKS 424
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:004888; F:transmembrane receptor activity; IEA.
 DR KW Receptor.
 SQ SEQUENCE 786 AA; 90290 MW; 1406C60FB5847F5B CRC64;
 QY Query Match 68.1%; Score 2830; DB 2; Length 786;
 Best Local Similarity 69.5%; Pred. No. 2.5e-168;
 Matches 540; Conservative 92; Mismatches 143; Indels 2; Gaps 1;
 Db 12 FHFVCMILIVGTRIOFSDGNEFADKSKGLIHPKDLPLKTYLMSQNYTBLQVS 71
 5 FHFATIFFMLIQIRIQSESEFLYDRSKNGLIIHVPDKLSQTTILINSONYISIWLTD 64
 QY 72 MSFLSLTIVRLSHRTOQLDLSVFKFDQDLEYLDLISHNOLQKISCHPVSFRHDLFSN 131
 : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
 Db 65 IISLSKRILILISHNRIOQYDLSVFKFDQDLEYLDLISHNOLQKISCHPVSFRHDLFSN 124
 QY 132 DFKAFLICKERGANLSQLNFIQNLQNLAMKQUDLPLAHHLHSYILDRLRNVIKENETSL 191
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 Db 125 AFDAFLICKERGANMQLKFLGILSTHLEKSVLPFLAHNLNPKVILVGEYGEKDP EGL 184
 QY 192 QILNAKTHLHVPHPSLFLAQNVNTSYNTGCOLNIK-LNDNCQVFRKLSLRTGS 249
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 Db 185 QDPNTESLHTVFPNKFPHFLDVSVKTVALELSNIKVLCEDNKCYSYFISLAKLQTNP 244
 QY 250 TIANFTLHETTWCCLVRLVQFLPMLPKPVETNNTIESIRBEDFTSKTALKI 309
 : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
 Db 245 KLSLSLTANNLTETWNFSRFLQVLMHTTWYPSISNVKQGQDLPFRDFYSGTSKALSI 304
 QY 310 BHITNOVFLFSQTAQLYTFSEMINMLTISDTPFHMLCHAPSPTFKFLNFTQVFTSDI 369
 : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
 Db 305 HQVSVTFGGFQPSVYIEVFSMUNIKNFTVSGTRWMTHMLCSKISLPFLHDFSNLITDVT 364
 QY 370 FERKCASTVKGELTTLQNGLKDPLKFGLMTRMPBLELLDVSWSNLESGRHENKTI 429
 : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
 Db 365 FENCGHILTELETLIQLQNLQNLKSLKAEMTQMKSLOQDLSQNSVYDEBKRGDCSWTKS 424
 QY 430 IWLNLSSNMITDSVRLPPIKVLQDHNSKIKSPKQVNLQELNVAFNSTLDP 489
 : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
 Db 425 ILSLNMSNLTIDTFRCLPPRKLVKDHLNSKIKSPKQVNLQELNVAFNSTLDP 484
 QY 490 GCGSFSSLVILIDANSVHSADFFOSCOQRISKAGDNPFQCTCLREVNIDQVS 549
 485 GCGSFSSLVILIDANSVHSADFFOSCOQRISKAGDNPFQCTCLREVNIDQVS 544
 550 EVLEGEDPSYKDYPESYRGSPKLDFHMSETISCNITLIVTGTATMLVLAUTVSLCYL 609
 545 EVLEGEDPSYKDYPESYRGSPKLDFHMSETISCNITLIVTGTATMLVLAUTVSLCYL 604
 Db 610 DLPWYLRMVCWTQTRRARNIPLEBLORNQPHAFYHSYRDHSANKSELVPLYKEDEDI 669
 605 DLPWYLRMVCWTQTRRARNIPLEBLORNQPHAFYHSYRDHSANKSELVPLYKEDEDI 664
 QY 670 QICLHERNFVGKSVENINCIKSYKSIPLSPNPNQVOSWCHYLYFAHNLFHEGSN 729
 Db 665 QICLHERNFVGKSVENINCIKSYKSIPLSPNPNQVOSWCHYLYFAHNLFHEGSN 724
 QY 730 NLLILLEPIQONSPNKYHKLAKMORTLQWPKRSKGFLFWANRAINKLT 786
 Db 725 SLILLEPIQYSIPSSYHKLKSMLARRTLEWPKEKSKGLFWANRAINKLT 781
 RESULT 12
 032MK4 HUMAN PRELIMINARY; PRT; 786 AA.
 ID 032MK4 - HUMAN PRELIMINARY; PRT; 786 AA.
 AC 032MK4;
 DT 06-DEC-2005, integrated into UniProtKB/TREMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DB Toll-like receptor 1.

QV 250 TLANFTLHETTCKCLYRFOELWPKPVYELNNTIESTREEDTSKUTKLALTI 309
 DR 245 KUSSLSTLNNTIETTWNFSFIRILQLQWHTTWYSSISNVKLUQGQDFRDYDSGTSKALSI 304
 DR 310 EHTINQVELFSQATALLYTSEMMINMLTSDTPRHMCPHAFSTFKLNFNTVWFDSI 369
 DR 305 HQTVNDVIGFPOSYIYFSNMNKNFTVSGTRNMHCPSKISPFHLDFDSNLITIV 364
 DR 370 FEKCSSTLVKLETTIQLQNGKLDLKFGVGLMTKDMPSLELUDVSNSNLSGRHKENTWES 429
 DR 365 FENGCHLIBLETLLQMNOKELSKIAENTTOMKSLQOLDISONSVSYDEKKGDCTSRS 424
 DR 430 IIVLNLSMMLTDSVRCPLPRKLDLHSNKJKSPKVQVKBLAQLNVAWSLTLP 489
 DR 425 LLSLMNSMNLDTTFRCLPPRKTFLVLDJNSNKTISPKQVVKBLAQLNVAWSLTLP 484
 DR 490 GCSSFFSISVLIDHNSVSHPSADFFQOCOMRSIKAGDNPFOCTCELERFVNIDQSS 549
 DR 485 GCGSFSSISVLIDHNSVSHPSADFFQOCOMRSIKAGDNPFOCTCELERFVNIDQSS 544
 DR 550 EYLEGWPSYKCDPESTRGSPKJDFHMSLSCNTLTLVITGATMULAVTWTLCYL 609
 DR 545 EYLEGWPSYKCDPESTRGTLKDFHMSLSCNTLTLVITVATMULAVTWTLCYL 604
 DR 610 DLWMLRMCQWOTRRARNPLBELORNQHAFASVHSAWVSELVYLERD 669
 DR 605 DLPYLRMVCQWOTRRARNPLBELORNQHAFASVHSAWVSELVYLERD 664
 DR 670 QICLHERNFVPGKSVENINCIEKSYKSIFVLSNPVFOSEWCHYELYFAHNLFHGSN 729
 DR 665 QICLHERNFVPGKSVENINCIEKSYKSIFVLSNPVFOSEWCHYELYFAHNLFHGSN 724
 DR 730 NULILUPIPIQONSPINKYKHLKALMORTYLOWPKESKRGFWANIRAFMMLT 786
 DR 725 SLILILUPIPIQOVSIPSYHKLSMARRTYLWPKESKRGFWANIRAINIKLT 781
 DR 239 IKPULSELTTRGSTLNFNTAHNTTCKLVRVPLWKPVELNTVNTIESTREEDPT 298
 DR 238 QNVLKLUQNSKLSNLNTANNITWNSPFTTQFWRTSIEFSVSSVKGQDDFRFD 297
 DR 299 YSKTAKLTHTIHITNQFLFQATALLYTVEFSMMNLTISTPFIHMCPRAPSTKFL 358
 DR 298 YSDTSLKALSHIQVSEVFSPQSYIVKIFSNNTIOVLTSAATHMVNVCPSQISPFLY 357
 DR 359 NFTONVFTDSIREBKSTLVKLETTIQLQNGKLDLKFGVGLMTKDMPSLELUDVSNSLEG 418
 DR 358 DESNNALTDWVFKNCANLNLITLQSLQMKELVNLVHMFEMOSLQQLDQSNTLYRD 417
 DR 419 RHKENCTWVESTVWLNSNMMTDSVRCPLPRKLDLHSNKKSPKQVKBLAQEL 478
 DR 418 ENBGSCITWTGSLSLNLSNLNTLDSVFRCLPPRKTFL 477
 DR 479 NTWAFNSLTDLPGGSFSSLSVLIDHNSVSHPSADFFQOCOMRSIKAGDNPFOCTCLR 538
 DR 478 NYASNLJAHLPCCGSFSSLNLIDNSISNSADFFQOCOMRSIKAGDNPFOCTCLR 537
 DR 539 EYVKNIDOVSSVTELEGMDPSYKCDPESYRSPPLKFHMSLSCNTLTLVITGATMUL 598
 DR 538 DFTQSLGQVSSVWESWPDPSYCEPESYKGTILKDFRVSLSNTALLLIVTGVGL 597
 DR 599 AVTVTSICVYLDPWYLMCQWOTRRARNPLBELORNQHAFASVHSAWVKS 658
 DR 598 ALWMTGLCQVYFPLWYMLCQWOTRRARNPLBELORNQHAFASVHSAWVKS 657
 DR 659 EYVPLERKEDQICLHERNFVPGKSVENINCIEKSYKSIFVLSNPVFOSEWCHYLYF 718
 DR 658 EYLPNVEKEGKICLCLHERNFVPGKSMENINCIIEKSYKSIFVLSNPVFOSEWCHYLYF 717
 DR 719 AHNLHFHEGSNNLILIDSPYQYSYHKLMAORTYLEPKESKIGLFWANR 778
 DR 718 AHNLHFHEGSNNLILIDSPYQYSYHKLMAORTYLEPKESKIGLFWANR 777
 DR GO; GO_0016020; C:membrane; IEA;
 DR GO_0004885; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR004075; IIL_rcpt_1.
 DR InterPro; IPR01611; LRR_C.
 DR InterPro; IPR00483; LRR_C.
 DR InterPro; IPR003591; LRR_C.

Fri Jun 9 14:07:34 2006

us-10-732-796a-12.rup

Page 16

Job time : 162 secs

GenCore version 5.1.9
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On protein - protein search, using sw model

Run on:

June 2, 2006, 22:53:30 ; Search time 22 Seconds
(without alignments)
3481.297 Million cell updates/sec

Title:

US-10-732-796a-12
Perfect score: 4154

Sequence: 1 MTKDKEPTVKSRHVFVCLMII.....IRAAFNNKLTLYTENNNDVKS 796

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2820	67.9	786	2	T88664
2	406.5	9.8	1097	2	A29943
3	285.5	6.9	1066	2	T15864
4	274	6.6	2	TR1387	
5	268.5	6.5	1039	2	T22117
6	268.5	6.5	1389	2	T13852
7	244.5	5.9	987	2	T0850
8	238	5.7	662	2	S42799
9	235	5.7	1531	2	T22118
10	233	5.6	1469	2	B46665
11	233	5.6	1480	2	A36665
12	230.5	5.5	921	2	B46234
13	226.5	5.5	559	2	T2998
14	225.5	5.4	1025	1	A37676
15	225	5.4	855	2	T07015
16	223	5.4	1091	2	A8532
17	221	5.3	1143	2	T10636
18	221	5.3	1692	2	A33988
19	5.3	560	2	A0164	
20	5.2	907	2	J30193	
21	5.2	572	2	T20947	
22	214.5	5.2	1134	2	T14587
23	212	5.1	853	2	T117461
24	211	5.1	661	2	I1662
25	210	5.1	890	2	E48486
26	210	5.1	2026	1	OYBY
27	208.5	5.0	983	2	G48524
28	207	5.0	800	2	H84740
29	5.0	1839	1	OYBYK	

ALIGNMENTS

RESULT 1

08664 Toll protein-like receptor DKEPZp54710610.1 - human
C;Species: Homo sapiens (man)

C;Accession: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
P;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, May 1999

A;Reference number: T08664
A;Accession: T08664

A;Molecule type: mRNA
A;Residues: 1-786 <POU>

A;Cross references: UNIPROT:Q15399; UNIPARC:UPI00016AC46; EMBL:AL050262
A;Experimental source: fetal brain; clone DKFZp54710610

C;Genetics:

A;Note: DKFZp54710610.1

Query Match 67.9%; Score 2820; DB 2; Length 786;
Best Local Similarity 69.4%; Pred. No. 3.1e-176;
Matches 539; Conservative 91; Mismatches 145; Indels 2; Gaps 1;

Qy	12	FHFVCLMIVIQTQIQPSDGFEPAVDKSKRGLIHVKVQDPLKTVKUDMSQNYIAEQVSD	71
Db	5	FHFVCLMIVIQTQIQPSDGFEPAVDKSKRGLIHVKVQDPLKTVKUDMSQNYIAEQVSD	64
Qy	72	MFLSELSTVLRUSHNRTOOLDSQVKENQDLYBDLSDHNOQTKISCHQPIVSFRHLSFN	131
Db	65	IISLSKRILITLISHNRQYDIBSVKENQEYLDLSDHNSKLVKISCHQPIVSFRHLSFN	124
Qy	132	DEKALPICKERGNLSDFNLGSLAMSKQKLUPIAHHSYVILLDRNYYTKENESTL	191
Db	125	AFDALPICKERGNMSQLKFLGLSTTHLEKSSVLPVIAHLNISKVLLVGETYGEKEDEGGL	184
Qy	192	QINAKTILHVTHPTSLPAQVNISTNGQLOTMK-LNDNQCVPIRSELTRGS	249
Db	185	QDFNTESLHVTPNKEFHFLDVSYVANLESLNKCVLBDSKCQSYFUSLAKLQNP	244
Qy	250	TIANFTNHNHTTWKCLVRVFOFLWPKPVNEYINYNTIESIREDPFTSYKTLKLU	309
Db	245	KLSSLTINNIEETWNFSPEIRILQWVWHITVWYSSISNUKQLODFDFDYSGTSLGAI	304
Qy	310	EHTINQFLFSOTALYVTFSENMIMMTISDTPFIRNLCPHAPSPTRFLNTONVTSDI	369
Db	305	HQVNSDVFVGFPQSYIVBIFSNMNKRNFTVSGTRVMHMLCPSKISPRHLDFSNNLTDV	364
Qy	370	PERKSTQVKLPLTLLQNLKDLFQGLMPLSFLLDVSWSLESGREKENCWVES	429
Db	365	FENCGHILTEFLLQNLKDLFQGLMPLSFLLDVSWSLESGREKENCWVES	424
Qy	430	IVVLNLSNMUDTSVFLPCKRIVKJDLHSNKIKSKPQVKVLEQBLNFAFNSLTDLP	489
Db	425	LISLNMSNLLDTFRCFLPPRKIVKJDLHSNKIKSKPQVKVLEQBLNFAFNSLTDLP	484

disease resistance
probable serine/threonine kinase
internalin protein
MEGF5 protein - rat
protein ACT-2 [impala]
hypothetical protein
orphan G protein-coupled receptor - t
Hcrgr-0 protein - t
ORF MSv257 leucine-rich repeat protein
hypothetical protein F20n2.4 [impala]
hypothetical protein
probable disease-related protein
probable receptor-hypothetical protein
chaoptin precursor

QY 490 GCGSFSSLVLIIDHNSVSHSADFFOSCOKRSIKAGDNPQCTCELRERVKNDQVS 549
Db 485 CGGSFSSLVLIIDHNSVSHSADFFOSCOKRSIKAGDNPQCTCELRERVKNDQVS 544
QY 550 EYLEGWDSDYKCDYDPESYRGPKLDFMSELSNCNTILLIVITGATMLVLAIVTTSIYL 609
Db 545 EYLEGWDSDYKCDYDPESYRGPKLDFMSELSNCNTILLIVITGATMLVLAIVTTSIYL 604
QY 610 DLWPWYRMRVCWQTCOTRRARNPLEELQRNQPHARTSYSSESDSAMKSVSEPYLLKED 669
Db 605 DLWPWYRMRVCWQTCOTRRARNPLEELQRNQPHARTSYSSESDSAMKSVSEPYLLKED 664
QY 670 QICLHERNFPVKSIVENIINIEKSYKSIFILSPNIVQSEWCHYELYFAHNLFHGSN 729
Db 665 QICLHERNFPVKSIVENIINIEKSYKSIFILSPNIVQSEWCHYELYFAHNLFHGSN 724
QY 730 NULILEPITOONSIPNKYKUKALMORTYQWPKRSKRGFLFWANIRAAFNKLT 786
Db 725 SLILILEPIQYSIPSSYHKUSIMARRTIVIEWPKRSKRGFLFWANIRAAFNKLT 781

RESULT 2

A29943 Toll protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A29943
R;Hishimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A;Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, ap
A;Reference number: A29943; MRID:80135760; PMID:2449285
A;Accession: A29943
A;Molecule type: DNA
A;Residues: 1-107 <HSA>
A;Cross-references: UNIPROT:P08953; UNIPARC:UPI000124803; GB:MI9969; GB:J02682; NID:915
A;Gene: FlyBase:Tl
A;Cross-references: FlyBase:FBgn0003717
C;Keywords: transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
Query Match 9.8%; Score 406.5; DB 2; Length 107;
Best Local Similarity 22.5%; Pred. No. 1.5e-18;
Matches 203; Conservative 145; Mismatches 321; Indels 235; Gaps 38;
QY 41 RGLIHLHPKD-----LPKTKVLDMSQNYIAELQVSDMSFLSILTIVRLSHRIQL 90
Db 160 RRLTHPPNLTDMDRNLSHLLRANTEEMPBLFDL-----NLESTFGSMKLRQ 211
QY 91 DLSVPRFKFNQDLEYLVDLPSHNOQKTSCH-----PTVSFRHL--- 126
Db 212 MPRGFKGKMPKLQKQLMWSNQHNLTKHDPEGATSVLGIDHDNGEQLPLDVFAHLTN 271
QY 127 ---DLSENDFKALP-----IKEFGNLSQMLFLGSAKML 158
Db 272 TDINLSANLFRSLPQGLFDHNRKHNLNEVRMLNNRVLPLTRPLRFQANPELQDILRRA-EL 330
QY 159 QKL-DLU-----PIAHHLISLILDRLRNYYKENETE-SQQLNAKTLHLYVHPFLSLFA 210
Db 331 QSLPGBLFEHSTQITNISLGNLNKLTPATLHEQVNLLSDLSNRLTH-----PDLSFA 387
QY 211 IQLNI-----SNTLGQIQLNTKLNDDNCQVFIKFELSELTRGSTL 251
Db 388 HTTNTLDRLLDNLUTGIGSGLFSNLGNLVLVMSRNRLRTIDSRAFS---TNGLRH 442
QY 252 INFTLHETTWKCLYRVFOLWPKVEY-----LNIYNNTI-----ESIRE 295
Db 443 LHDHNDIDLOQPLDMDLQTOINSPEGGYMGMLLTNLRNNSLIFYNDWMNTMLQREL 502
QY 296 DFTYSKTLKALTIEHTINQVFLFSQTALYTF-----EMIMML 336

RESULT 3

T15864 hypothetical protein_C56B6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15864
R;Fulton, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C56B6.
A;Reference number: S69019
A;Accession: T15864
A>Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1066 <PUT>
A;Cross-references: UNIPROT:Q18902; UNIPARC:UPI0000811D7; EMBL:U39996; NID:91055114; PIU
A;Genetics: C56E6.6
A;Gene: C56E6.6
A;Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 833/3; 892/3; 9
Query Match 6.9%; Score 285.5; DB 2; Length 1066;
Best Local Similarity 21.0%; Pred. No. 1.1e-10;
Matches 140; Conservative 123; Mismatches 220; Indels 185; Gaps 30;
QY 21 IVGTRIQPSDNEFAVDKSKRGLIHVPKDPLKTKVLDMSQNYIAELQVSDMSFLSILTIV 80
Db 421 LAGNQDIDTENMFQSSSS-----ELSNLNLHKNHSRSFSFDLNLQO 468
QY 81 LRLSHHRQLQDLSYFKNDLEYDLSHNLQKLSCH-----PTVSFRHL----- 127
Db 469 LRISHNIRITTSMSFLNRLNRYLDLSHNRKIKLPSALYQPLDVLHLDHNLNEID 528
QY 128 -----LSFENDFKAFLP-----CKEGNLSQMLFLGIGSAMKQKLDPPIAHHLHSYI 174
Db 529 RDAFRSFSDLQSLKUSHNAFRRFSCFELJSISQHOLDISNQINEIDFCIAR----- 582

A; Molecule type: mRNA
A; Residues: 1-1389 <ELD>
A; Cross-references: UNIPROT:Q24591; UNIPARC:UPI000007A826; EMBL:L23171; NID:g415682; PIH
C; Genetics:
A; Gene: wheeler
A; Cross-references: FlyBase:FBgn0004364

F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;552-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;620-633/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;653-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;701-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;841-880/Domain: proteoglycan carboxyl-terminal homology <EGF>
F;1038-1051/Domain: EGF homology <EGF>
F;11088-11091/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

Query Match 5.6%; Score 233; DB 2; Length 1469;
Best Local Similarity 18.9%; Pred. No. 4.7e-07;
Matches 170; Conservative 112; Mismatches 293; Indels 326; Gaps 31;

Qy 36 VDKSKKGILIHVKDPLUKTKVLDMSONYALQVSMSFLSRLTIVLRLSHRIQLDLV 95
Db 84 VDCSHRGILSVPRKISADVERLEQGNNLTIVYETDFQLRKLMLQLTDQIHTERN 143
Qy 96 PFKENQDLEYLDLISHNQLQKISCHPI--VSFRHLDLSFNDFKALPICKERFSNLQSNFLG 152
Db 144 FQDLVSLERLQJLQINNNTTIVRVEPKAQSRSQIQLDNQITC-----LDEAFKG 194
Qy 153 ISAMKLUQLDILIPIAHLHLSVILLDRNYYKENETESLQIQLNAKTLHLVHFPTSHFAIQ 212
Db 195 L-----VELEITLNNNNLTSPLPHNF--- 216
Qy 213 UNISVNTLGCLQLTNIKLNNDNCQVFKEFLRLTRST-LANFTLHETTWKLCLRVFQ 271
Db 217 ----GGIGRLRALRISDNPPACDHLSWLSRFLSATRMAPY-----RCQS---- 259
Qy 272 FLWPKEVYLINYNTIESREEDFTYSKTKLA----- 306
Db 260 ---PSQIKGQVADL-----HQDQFCKSGIHEAPMECGAENGSCPHPCRGADGIVDCRE 310
Qy 307 -----LTIRHITNQVLFQSFQTALEYVFSNNIMMLTISDTPFIRLCPRAPISTKFL- 358
Db 311 KSLTSVPUVTPDDTTPVRL-----SON-----FTBLPPGSFSSFRRLR 349
Qy 359 -----NFTONVFTISFEKSTVLKLETLLQKNGKDL---PRVGLMT----- 399
Db 350 RIDLSNNNISRTAHDALSGLKQLTTLVLYGKHKIKOLPLSGVFR-GLGSLRLILLNABISC 408
Qy 400 -----KDMPSLIELVWSNLES----- 417
Db 409 IRKDAFRDHLSSLSLYDNNNIOSSLANGTEDAMKSMKVHAKNPKICDCMCLRLADYLH 468
Qy 418 -----GRHKENTWTSIVVN----- 434
Db 469 RNPPIETSGARESPKRMRRIKESLREBKFKCSWGLRMKUSGECRMDSDCPAMCHCEGT 528
Qy 435 -----LSSNML---TDSVFRCLPPRKVLDLHSNKSV- 465
Db 529 TWDCTGRRKLTPRDIPLHTTELLNDNEGRISSDGFLGRPLHKL-LELKRNLGTIE 587
Qy 466 PKQVVKVLEALQELNVAFNLSLDPG-CGSSSSLVIIDNSVSPSADFQSCOKRS 523
Db 588 PNAFBGASHIQOBLQZGKINGKBNKISNMFLGHQKLNLYNOIQCVPSEPHANLTS 647
Qy 524 IKAGDNPFQCTCELREFPKVNDQVSVBVELEGWPDSYKCDYPSYRSQSPKDFHMSBLCN 583
Db 648 INLASLNPFCNCHLAWFAEYTRKS---LNG---GAARGGASKVROVQIKOLPHBFKCS 702
Qy 584 ITLLIVITGATMVLIAVTUTSCLYIDLPWVILRMQWTOTARRNPIEFLORNLQFH 643
Db 703 SENSEGCLGDQYCPCPSCCTGTV-----ACSRNQKJKEIPRGIPAE----- 743
Qy 644 AFISYSEHDSAWKSLVPUYRKEPIQICLHERNFVPGKSVENT--INCXKSYKSFV 701
Db 744 -----TSEL-YVSENEEQIHW-----IRHRSLSTRIDLSNNQITI '780

RESULT 11
A36665 slit protein 1 precursor - fruit fly (*Drosophila melanogaster*)
Qy 702 LSPNFWOSEWCHVELYFAHHNIFH-----EGSNVILILLEPIQONSIP-NKYKLUKA 753
Db 781 LS-NYTFANTLKLSTLISYNKLQCLQRHALSGANNRUVSLHGNRISMLPEGSEFDLKS 839
Qy 754 L 754
Db 840 L 840

C;Species: *Drosophila melanogaster*
C;Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: A36665; UniProt:UPI000150FD1; PIDN:CAA37910_1; PID:98
P;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit, an extracellular protein necessary for development of midline glia and cc
A;Reference number: A36665; MOLID:91099665; PMID:2176636
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-1480 <ROT>
A;Cross-references: UNIPARC:UPI000150FD1; GB:M23543; NID:8340939; PID:9514357
C;Genetics:
A;Gene: FlyBase:Sl1
A;Cross-references: FlyBase:FBgn0003425
A;Introns: 135/13
C;Superfamily: fruit fly slit Protein; EGF homology; leucine-rich alpha-2-glycoprotein r
C;Keywords: alternative splicing; growth factor
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;322-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;701-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;845-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1038-1051/Domain: EGF homology <EGF>
F;11088-11091/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

Query Match 5.6%; Score 233; DB 2; Length 1480;
Best Local Similarity 18.9%; Pred. No. 4.7e-07;
Matches 170; Conservative 112; Mismatches 293; Indels 326; Gaps 31;

Qy 36 VDKSKGLIHVVKDPLUKTKVLDMSONYALQVSMSFLSRLTIVLRLSHRIQLDLV 95

Nature 408, 816-820, 2000
 A; Authors: Hunter, J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; M.
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Iuro, S.; Uversky, V.; Vandevert, C.;
 A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.;
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venier, J.C.; Davis, R.W.;
 A; Title: Sequence and analysis of chromosome 1 of the Plant Arabidopsis.
 A; Reference number: A86141; MUID:21016719; PMID:11130712
 A; Accession: B86234
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-921 <STO>
 A; Cross-references: UNIPROT:004517; UNIPARC:UPI000048210; GB:AE005172; NID:9216
 C; Genetics:
 C; Superfamily: Receptor-like protein kinase
 Query Match 5.5%; Score 230.5; DB 2; Length 921;
 Best Local Similarity 21.5%; Pred. No. 3.7e-07;
 Matches 172; Conservative 137; Mismatches 317; Indels 175; Gaps 39;
 QY 50 LPLKTKVLDNSQNYTAELQDSDMSFL-SELTIVLRLSHNRICOLLOLDSVEKFENQDLYLDS 108
 Db 311 KSLTSVPVTLDDTDVRL--EQN-----FTELPKSFSSFRRLR 349
 QY 359 --NFTQNVFDSDIFFKCSLTVLKLETILQKNGKLQI---FKVGMNT----- 399
 Db 350 RIDLSNNNISRRAHDALSGKLQKTTIVLYGKRNKIKULPSGVFK-GIGSLRLILLNNABISC 408
 QY 400 -----KDMPSLEIDLVWSLSES 417
 Db 409 IRKDAFRDLHSLSLSLYDNIQSTANGTEDAMKSMTKVLAKNPICDCNTRWADYLH 468
 QY 418 -----GRHKENCTWESIVVNN----- 434
 Db 469 KNPKETSGARCESPGRMHRRIIESRREEBKFKCSWQBLRMKLSGECRMDSDCPAMCHCEGT 528
 QY 435 -----SSNML---TDSVRCFLPPRKVLUKDHNSNKKSV- 465
 Db 529 TVDCTGRRKLKEIPRDIPLHTELLNDNELGRISSTGFLGRPLHYK-LELKRNLQTGIE 587
 QY 466 PKQVKLEALQELNATPNSLTDLPG--CGFSSSLVLTIDHNSVSHPSADFFQSCQKMR 523
 Db 588 PNAFFGASHIQELQNGENKIKEISKMKFLGHQKLTINLYDNOISCPMPSESFHNSLTS 647
 QY 524 IKAGBNPFOOTCCELBKFVKQIDQVESEVLCGWPDSKCDYPSVYGSPLKDFHMABLSCN 583
 Db 648 LNLAASNPNENCLHAWFAECURKGS--LNG--GARCGAPSJKVQDVKOLPHSBFKCS 702
 QY 584 ITLITVTIGATMLVIAVTSLCITLDLPMWLRMWCQWTQRRARNPIEELQNLQFH 643
 Db 703 SENSGCGLDGYCPCPSCCTGTVV-----ACSRNQIKEIPRGIPAB----- 743
 QY 644 AFISYSEHDSAWVKSLVPLKEIQICLHERNFPVGKSIVENI--INCIEKSKSIVF 701
 Db 744 -----TTEL-YLESNLIEQIHYR-----IRHRSLRUDLSNQQT 780
 QY 702 LSPNIVVOSEWCHYELYFAHNLFH-----EGSNNLILITLEPFPONSP--NKTKHLKA 753
 Db 781 LS-NTFANILTKLSTLISYNKLOCLRHALSGLMNLRVSLHGKRISMPEGSFEDLKS 839
 QY 754 L 754
 Db 840 L 840

RESULT 12

B86234 hypothetical protein [imported] - *Arabidopsis thaliana*
C. species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02 Mar-2001 #text_change 31-Dec-2004
C; Accession: B86234
R-Theologis, A.; Baker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.H.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.P.; Hughes, B.; Huijari, L.

QY 153 LSAMKLQKUDLPLPAHLHSYIILDLRNYYIKENETESQOLNAKTILHVHPFLSAIQ 212
 Db 195 L----- 216
 QY 213 VNTSVNTGCOLTNTKLNDDNCOVFIKELSELTRGST-LINFTNHIERTWKCVLVRVQ 271
 Db 217 -----GGGLRRAIKRUSDNPFACDCHLSWLSRFLRSATRAMP-----RCQS--- 259
 QY 272 FLWKKPVEMINTYNTIESIREEPTYSKTLK 306
 Db 260 ---PSQLKGONVADL----HDOPFKCSLTERHA.PMECGAENS.CPHPCRCADCIGDVCRE 310
 QY 307 -----LTIEHTIMQVFLFSQTALEYTIVFSEMINMILTISDTPFTHMLCHAPSTPKFL- 358
 Db 311 KSLTSVPVTLDDTDVRL--EQN-----FTELPKSFSSFRRLR 349
 QY 359 --NFTQNVFDSDIFFKCSLTVLKLETILQKNGKLQI---FKVGMNT----- 399
 Db 350 RIDLSNNNISRRAHDALSGKLQKTTIVLYGKRNKIKULPSGVFK-GIGSLRLILLNNABISC 408
 QY 400 -----KDMPSLEIDLVWSLSES 417
 Db 409 IRKDAFRDLHSLSLSLYDNIQSTANGTEDAMKSMTKVLAKNPICDCNTRWADYLH 468
 QY 418 -----GRHKENCTWESIVVNN----- 434
 Db 469 KNPKETSGARCESPGRMHRRIIESRREEBKFKCSWQBLRMKLSGECRMDSDCPAMCHCEGT 528
 QY 435 -----SSNML---TDSVRCFLPPRKVLUKDHNSNKKSV- 465
 Db 529 TVDCTGRRKLKEIPRDIPLHTELLNDNELGRISSTGFLGRPLHYK-LELKRNLQTGIE 587
 QY 588 PNAFFGASHIQELQNGENKIKEISKMKFLGHQKLTINLYDNOISCPMPSESFHNSLTS 647
 Db 524 IKAGBNPFOOTCCELBKFVKQIDQVESEVLCGWPDSKCDYPSVYGSPLKDFHMABLSCN 583
 Db 648 LNLAASNPNENCLHAWFAECURKGS--LNG--GARCGAPSJKVQDVKOLPHSBFKCS 702
 QY 584 ITLITVTIGATMLVIAVTSLCITLDLPMWLRMWCQWTQRRARNPIEELQNLQFH 643
 Db 703 SENSGCGLDGYCPCPSCCTGTVV-----ACSRNQIKEIPRGIPAB----- 743
 QY 644 AFISYSEHDSAWVKSLVPLKEIQICLHERNFPVGKSIVENI--INCIEKSKSIVF 701
 Db 744 -----TTEL-YLESNLIEQIHYR-----IRHRSLRUDLSNQQT 780
 QY 702 LSPNIVVOSEWCHYELYFAHNLFH-----EGSNNLILITLEPFPONSP--NKTKHLKA 753
 Db 781 LS-NTFANILTKLSTLISYNKLOCLRHALSGLMNLRVSLHGKRISMPEGSFEDLKS 839
 QY 754 L 754
 Db 840 L 840

QY 648 YSEHDSAWVKSLVPLKEIQICLHERNFP-----PGKSVIENIINC- 691
 Db 649 -----KHEWSIKSFRRKOMSTEDDIDSKEENLIGGGGGDVVVFQGDKEVAKHRCSS 671
 QY 614 --KHEWSIKSFRRKOMSTEDDIDSKEENLIGGGGGDVVVFQGDKEVAKHRCSS 671
 Db 692 TEKSYKSF-VLSPNIVVOSEWCHYELY---FAHNLF---HEGSNNLILILLEIPQN 742
 QY 672 TOKNFSSAMPFLITERGRSKFETEVOTLSSIRHINVKUCSITSDDSLVUYLPNG 731

Qy 743 SPPNKVHKULKALMTOYILOW 763
 | : | | | | | | | | | | | | | | | | |
 : : | | | | | | | | | | | | | | | | |
 : : | | | | | | | | | | | | | | | | |
 Db 732 SLWDMHLHSCK----KSNLGN 747

RESULT 13

T42998 Ras-binding protein SUR-8 - *Caenorhabditis elegans*
 N:Alternate names: leucine-rich repeat protein
 C:Species: *Caenorhabditis elegans*
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T42998
 R;Seljors, L.M.; Schutzman, J.L.; Borland, C.Z.; Stern, M.J.
 Proc. Natl. Acad. Sci. U.S.A. 95, 6503-6508, 1998
 A>Title: Soc-2 encodes a leucine-rich repeat protein implicated in fibroblast growth fac
 A;Reference number: 222280; MUID:98284030; PMID:961851
 A;Accession: T42998
 A;Strain: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-559 <SPL>
 A;Cross-references: UNIPROT:Q22875; UNIPARC:UPI0000083557; EMBL:AF054827; NID:93293317;
 R;Sieburth, D.S.; Sun, Q.; Han, M.
 Cell 94, 119-130, 1998
 A:Title: SUR-8, a conserved Ras-binding protein with leucine-rich repeats, positively re
 A;Reference number: 222331; MUID:98337190; PMID:9674433
 A;Accession: T43192
 A;Strain: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-559 <SPL>
 A;Cross-references: UNIPARC:UPI0000083E57; EMBL:AF068919; NID:93252976; PIDN: AAC39129_1;
 A;Gene: soc-2

Query Match 5.5%; Score 226.5; DB 2; Length 559;
 Best Local Similarity 22.2%; Pred. No. 3.5e-07;
 Matches 133; Conservative 106; Mismatches 196; Indels 105; Gaps 28;
 A:Title: SUR-8, a conserved Ras-binding protein with leucine-rich repeats, positively re
 A;Reference number: 222331; MUID:98337190; PMID:9674433
 A;Accession: T43192
 A;Strain: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-559 <SPL>

Query Match 5.5%; Score 226.5; DB 2; Length 559;
 Best Local Similarity 22.2%; Pred. No. 3.5e-07;
 Matches 133; Conservative 106; Mismatches 196; Indels 105; Gaps 28;
 A:Title: SUR-8, a conserved Ras-binding protein with leucine-rich repeats, positively re
 A;Reference number: 222331; MUID:98337190; PMID:9674433
 A;Accession: T43192
 A;Strain: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-559 <SPL>
 Query Match 5.5%; Score 226.5; DB 2; Length 559;
 Best Local Similarity 22.2%; Pred. No. 3.5e-07;
 Matches 133; Conservative 106; Mismatches 196; Indels 105; Gaps 28;
 A:Title: SUR-8, a conserved Ras-binding protein with leucine-rich repeats, positively re
 A;Reference number: 222331; MUID:98337190; PMID:9674433
 A;Accession: T43192
 A;Strain: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-559 <SPL>

Qy 497 LSVLIDINNSVSHPSADFFQSCQKMSIKAGDNPFQCTCELREFVNIDQSVSEVLEGWP 556
 | : | | | | | | | | | | | | | | | | |
 : : | | | | | | | | | | | | | | | | |
 : : | | | | | | | | | | | | | | | | |
 Db 492 LKSLYNDNSLHNTLPPEALCQSLEMSIENSP-----LSQDIPPEITAGGP 558

RESULT 14

A57676 protein kinase Xa21 (EC 2.7.1.-), receptor type precursor - rice
 C:Species: *Oryza sativa* (rice)
 C:Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 31-Dec-2004
 C:Accession: A57676
 R;Song, W.Y.; Wang, G.L.; Chen, L.L.; Kim, H.S.; Pi, L.Y.; Holster, T.; Gardner, J.; War
 Science 270, 1804-1806, 1995
 A>Title: A receptor kinase-like protein encoded by the rice disease resistance gene, Xa21
 A;Reference number: A57676; MUID:96106403; PMID:8525370
 A;Accession: A57676
 A>Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Strain: type; DNA
 A;Residues: 1-1025 <SPL>
 A;Cross-references: UNIPROT:Q46640; UNIPARC:UPI0000A2DFF; GB:U37133; NID:9122442; PID:
 C:Keywords: Atp; glycoprotein; magnesium; phosphotransferase; receptor; serine/threonine
 A;Note: confers resistance against the bacterial pathogen *Xanthomonas oryzae* pv. *oryzae*
 C:Superfamily: Receptor-like protein kinase
 C:Genetics: Xa21
 F:1-123/Domain: signal sequence #status predicted <SIG>
 F:124-1025/Product: protein kinase Xa21 #status predicted <MAT>
 F:80-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology
 F:104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:225-248/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:249-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:274-297/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:298-321/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
 F:322-345/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F:346-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F:377-401/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
 F:401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F:425-448/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F:449-472/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
 F:473-496/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
 F:498-521/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
 F:522-545/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
 F:546-569/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
 F:570-593/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
 F:594-618/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
 F:706-1011/Domain: protein kinase homology <KIN>
 F:714-722/Region: protein kinase homology <KIN>
 Db 169 IHLISYLTIDILDRYY-----IKNENETSLQQLNAKTHLHVPIHTSLFAIONTIVLGC 222
 Qy 221 NHLLTRYPEEIGGCHSLTQLDIHDNLSELPELPSIGKLNLV-----RIGIRYKIRC 271
 Db 223 IQLNTNKLNDNCQEVTFKELSTLRESTLNLINLTNLHETTKCLVNFQEWPKPVYN 282
 Qy 272 -----IPSELSBSCQLEBFIVE-----SNHL-----QLLP-----N 298
 Db 283 TYNLTTIESIREBDFTYSKT-----LKLATIEHTINQVF-----LFSQATALYT 327
 Db 299 I-----LTMPLKPTIUNLNLERNLTAFFPAGSPQOQFVSTVTINGNENIQISKIPIGESKA---TR 353
 Qy 328 PSEMNTMLTISDTPFTHMLCPHAPSPTKFLENFT-----VFDTSIFBKCSFLVKLFL 384
 Db 354 I-----LTMPLKPTIUNLNLERNLTAFFPAGSPQOQFVSTVTINGNENIQISKIPIGESKA---TR 405
 Qy 385 QNGLKDLF-FKVGLMTKDMRPLSLEBILQDLYWSWNALIESGRHKENTTWESIVVLLNLSNLIDS 443
 Db 406 SNNQLKKLGPQNQIGNLK-----LRELDLENELET----- 435
 Qy 444 VFLCFLPPIRKVND-----LHSNKKKSVPKQVVKALEQELNVAFLNVSLSLTDIP-GCCSFSS 496
 Db 436 -----VPEIIGFQHLLTKLUWVSNKILTPRSIGNLCSLQDIDRGENNLTAAPEEICHLDS 491
 Qy 203 -----FH-----PTS-----LPAIQV--NI--SVNTLQCLQTNI-----KLND 232

QY 233 DNCQVF1KFLSELTRGQSTLNFNTINHIELTWKCLVRFQFLWPKEVEYLINYLTIESI 292
 Db 340 D----WGPVISDLTNCNSKLQ-TUNLGERN-----;LGGV 366
 QY 293 REBDFTYSKTTK-AUTEHTINQVFLFSQTALEYTVFSEMINIMLTISDTPFTMLCPH 350
 Db 367 LEPNSFSNLSTSFLAELINKTGSI-----;PDKIGNULIGLQLHLQNFRGLS-PS 418
 QY 351 ABSTFKFLNFT--QNVFTDSIFERKSTVLFETLORN-----GLKDLFKVG 396
 Db 419 SLGRLKNGILLAYENNLNSGSIPIAIGNTELNLLILGINKFSGWIPYTSNLNLISLG 478
 QY 422 ENTWKVESTIVNLNSNMIDSVRFLCP-PRIKUDLHSNKIK-SVPKQVVKBALQEL 478
 QY 427 LMFKDM----PS-----LEI-LDVSNLSE-----;SGRHK 421
 Db 479 LSTTNLSPGIPSELPNLNQTSIMIVNSKONLEGSTPOEICLHLKNLVEFHAESENRLSLGKIP 538
 QY 539 NTLGDCQFLRYLVLYCQNNLJGSIPLSAGQKGLEFLDLSNNLSQLPISLADTMHSL 598
 QY 479 NVAFLNSLT-DLRGCGCSFSSLVSLVLDHNSVSHPSADFFQSCQMRISIAGDNPFQCTCEL 537
 Db 599 NLFSNSFVGVEPTTGAFAKASGSIQGN-----;LGGV 366
 Db 538 REPVKNIQVSSEVLELEGWPSYK---CDYPSYRGSPKDFHMSLSCNLTIVTIGAT 594
 QY 627 -----AKUGGGPDILPRCPCPPLLENKRHP-----;VLPIVSLLAA 663
 QY 595 MVLAVNTVSLCIVLDLFWYLRLMWCQWTQTRRAKNPILPELORNLQHFHAFIS----- 649
 Db 664 LATLS-----SLYLITWHKR-----TKKGAPS-----RSMKGHLVSQLVKA 704
 QY 650 -----;EDHSAWKSEBLVPLYEKEIOIC-----IHERNF 678
 Db 705 TDGFAPTPNLGSSGFGSVVKGKLNQDHAVKVKLGENPGALKSTAECAALRNHRHL 764
 QY 679 VPKSISVENIINCIEKSYKSIFVLSPNFVQSEWCHE 715
 Db 765 VKITVTCSSIDNRGNDFKAVYDFMPNGSLEDWIHPE 801

RESULT 15
 T07015
 Cf-4A protein - tomatoo
 C;Species: Lycopersicon esculentum (tomato)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T07015
 R;Takken, F.L.; Schipper, D.; Nijkamp, H.J.; Hill, J.
 Plant J. 14, 401-411, 1998
 A;Title: Identification and Ds-tagged isolation of a new gene at the Cf-4 locus of tomato
 A;Reference number: Z15863; MUID:98335213; PMID:9670557
 A;Accession: T07015
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-855 <TAK>
 A;Cross-references: UNIPROT:O50024; UNIPARC:UPI000009FC28; EMBL:Y12640; NID:e1289424; PI
 A;Experimental source: strain Cf-4; isolate MM-Cf-4
 A;Genetics:
 A;Gene: Cf-4A
 A;Map position: 1

Query Match 5.4%; Score 225; DB 2; Length 855;
 Best Local Similarity 23.6%; Pred. No. 7.6e-07;
 Matches 123; Conservative 84; Mismatches 176; Indels 138; Gaps 25;
 QY 105 LDLSHNLQLO-----KISCHPIVSPFHFDLSFNDFEALPICKEGFLNLSQL-----NLF 151
 85 LDLGCSQLOGKFFHNSNLSFOLNSNLRKLDISNDFFGSPISPKFGRSDLTHLDISDSNFT 144
 QY 152 GLSAMKLUQKLDPPIAHLHISYL-----LDIARY-YIKENESTESLQLNAXTILHLV 202

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OM protein - protein search, using sw model

Run on: June 2, 2006, 22:52:45 ; Search time 107 Seconds
(without alignments)

3401.348 Million cell updates/sec
US-10-732-796A-12

Title: Perfect score:
Sequence: 1 MTKKEPTIVSKFHVCLMII.....IRAAFNMKLTIVTENNDVRS 796

Scoring table: BL05IM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 sqqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 8;*
1: geneseq1980s;*
2: geneseq1990s;*
3: geneseq2000s;*
4: geneseq2001s;*
5: geneseq2002s;*
6: geneseq2003as;*
7: geneseq2003bs;*
8: geneseq2004as;*
9: geneseq2005as;*
10: geneseq2006s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4154	100.0	796	8 ADP56660	Adp56660 Human Tol
2	4154	100.0	796	8 ADP48601	Adp48601 Human Tol
3	4154	100.0	796	8 ADU23189	Adu23189 Human Tol
4	4149	99.9	796	5 Ael16109	Ael16109 Human DNA
5	4149	99.9	796	8 ADU23188	Adu23188 Human Tol
6	4149	99.9	796	8 ADU23190	Adu23190 Human Tol
7	4149	99.9	796	9 ADX06216	Adx06216 Cyclin-de
8	4143	99.7	796	3 AYB8054	Ayb8054 Human Tol
9	4048	97.4	780	5 AEL16112	Ael16112 Human DNA
10	4021	96.8	781	4 AUU25469	Auu25469 Human mdd
11	3144.5	75.7	795	8 ADU23197	Adu23197 Murine Tol
12	3144.5	75.7	806	8 ADU23195	Adu23195 Murine Tol
13	3139.5	75.6	806	3 AAY8055	Aay8055 Murine Tol
14	3139.5	75.6	806	8 ADU23194	Adu23194 Murine Tol
15	3139.5	75.6	806	8 ADU23196	Adu23196 Murine Tol
16	2830	68.1	786	2 AAW82349	AAW82349 Human DNA
17	2830	68.1	786	5 AAE16090	Aae16090 Human DNA
18	2830	68.1	786	7 ADC78821	Adc78821 Human PRO
19	2830	68.1	786	7 ADE25535	Ade25535 Human rel
20	2830	68.1	786	8 ADP56650	Adp56650 Human Tol
21	2830	68.1	786	8 ADP48591	Adp48591 Human Tol
22	2830	68.1	786	8 ADP4896	Adp4896 Human PRO
23	1905.5	45.9	811	2 AAY05868	Aay05868 Human Tol

ALIGNMENTS

RESULT 1	ID	ADP56660 standard; protein: 796 AA.
XX	XX	AC
XX	XX	ADP56660;
DT	09-SEP-2004	(first entry)
XX	DR	Human Toll-like receptor TIR6 protein - SEQ ID 12.
XX	KW	expression system; Toll-like receptor; TIR6; immune response modifier; IRM; cancer; gene therapy; human; receptor.
XX	OS	Homo sapiens.
XX	PR	WO2004053057-A2.
XX	PN	WO2004053057-A2.
XX	PD	24-JUN-2004. /
XX	PF	31-OCT-2003; 2003WO-US034563.
XX	PR	11-DEC-2002; 2002US-0432651P.
XX	PA	(MINN) 3M INNOVATIVE PROPERTIES CO.
XX	PT	Gupta SK, Ghosh TK, Fink JR;
XX	DR	WPI; 2004-468833/44.
XX	N-PSDB;	ADP56659.
XX	PT	New expression system comprising a first nucleic acid sequence that encodes a Toll-like receptor (TLR), useful for preparing a composition comprising TLR agonist for treating e.g., cancer.
XX	PT	The invention relates to a novel expression system comprising a first nucleic acid sequence that encodes a Toll-like receptor (TLR). Operably linked to a first expression control sequence and a second nucleic acid sequence that encodes a reporter. TLRs are immune response modifiers (IRMs). The expression system of the invention may be useful for preparing a composition comprising the TLR agonist for treating cancer, possibly via gene therapy. The current sequence is that of the human Toll-like receptor TLR6 protein (SEQ ID 12) of the invention.
XX	CC	Sequence 796 AA;
XX	CC	Aay66644 Membrane-
XX	CC	Aau29230 Human PRO
XX	CC	Aab65167 Human PRO
XX	CC	Ael16108 Human DNA
XX	CC	Abu58606 Human PRO
XX	CC	Abu8154 Novel hum
XX	CC	Abu84469 Human sec
XX	CC	Abre66343 Human sec
XX	CC	Abre5733 Human sec
XX	CC	Abu9673 Human sec
XX	CC	Abu57982 Human PRO
XX	CC	Abu59060 Novel hum
XX	CC	Abu82572 Human sec
XX	CC	Abu82912 Human PRO
XX	CC	Abu90033 Novel hum
XX	CC	Abre68282 Human sec
XX	CC	Abu60491 Human sec
XX	CC	Abu933 Novel hum
XX	CC	Abu92766 Human sec
XX	CC	Ab008843 Human sec
XX	CC	Ab002895 Human sec
XX	CC	Ab075049 Human sec

Query Match 100.0%; Score 4154; DB 8; Length 796;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 796; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 MTKDKEPIVKSFHVCLMIIIVGTRIQFSDENEFAVDKSKEGLIHPKDLPLKTKVLDMS 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 1 MTKDKEPIVKSFHVCLMIIIVGTRIQFSDENEFAVDKSKEGLIHPKDLPLKTKVLDMS 60
 XX
 Db 61 QNYIAELQVSMSFSELTVRLSHRIQQLDSVFKFDLEYIDLSHNOLOKISCHPI 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 61 QNYIAELQVSMSFSELTVRLSHRIQQLDSVFKFDLEYIDLSHNOLOKISCHPI 120
 XX
 Db 121 USFRHDLDFNDFKALPICKFGNLSQNLFIGLSAMKLQKUDLPIAHHSYILDNR 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 121 USFRHDLDFNDFKALPICKFGNLSQNLFIGLSAMKLQKUDLPIAHHSYILDNR 180
 XX
 Db 181 YYIKENETESIQLINAKTILHIVFHPTSLFAIQNLQVNTGCOLTNIKUNDNNQVFIR 240
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 181 YYIKENETESIQLINAKTILHIVFHPTSLFAIQNLQVNTGCOLTNIKUNDNNQVFIR 240
 XX
 Db 241 FSELTRGLSTLNFTNHIEITWKCIVRVRVQFLPKPVENYIYLIESIREDDFTYS 300
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 241 FSELTRGLSTLNFTNHIEITWKCIVRVRVQFLPKPVENYIYLIESIREDDFTYS 300
 XX
 Db 241 FSELTRGLSTLNFTNHIEITWKCIVRVRVQFLPKPVENYIYLIESIREDDFTYS 300
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 241 FSELTRGLSTLNFTNHIEITWKCIVRVRVQFLPKPVENYIYLIESIREDDFTYS 300
 XX
 QY 301 KITLKALTIEHTNQVPLFSQTAIYVFSENMIMLITISDTPPIHLCPHAPSTKFPLN 360
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 301 KITLKALTIEHTNQVPLFSQTAIYVFSENMIMLITISDTPPIHLCPHAPSTKFPLN 360
 XX
 Db 361 TQNVFDTSIFRKCSITLVKLETILQKNGKLQFLKVSLMTKOMPSBILDYWSNLSGRH 420
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 361 TQNVFDTSIFRKCSITLVKLETILQKNGKLQFLKVSLMTKOMPSBILDYWSNLSGRH 420
 XX
 Db 421 KENCTWVESTVTLNSNSNMLTDSVFCVCLPPRKVLDLHSNIKSVKVKVLEAQELNV 480
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 421 KENCTWVESTVTLNSNSNMLTDSVFCVCLPPRKVLDLHSNIKSVKVKVLEAQELNV 480
 XX
 Db 481 AFNSLTDLPGCGSFSSLSVLTIDHNSVSHPSADFFOSCQKRSIKAGDNPFQCTCELREF 540
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 481 AFNSLTDLPGCGSFSSLSVLTIDHNSVSHPSADFFOSCQKRSIKAGDNPFQCTCELREF 540
 XX
 Db 541 VKNIDQVSSEVLEGWDSYKDYPESYRGSLKDFFMSLSCNITILLIVGATMVLAV 600
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 541 VKNIDQVSSEVLEGWDSYKDYPESYRGSLKDFFMSLSCNITILLIVGATMVLAV 600
 XX
 Db 601 TVTSICLYLDIPWYLRMWCQHOTRBRARNPLPEELQRTNQPHAFISYSESDSAWYSEL 660
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 601 TVTSICLYLDIPWYLRMWCQHOTRBRARNPLPEELQRTNQPHAFISYSESDSAWYSEL 660
 XX
 Db 661 VPYLEKEDIOCLHERNFVPCKSIVENIINCIEKSYKISFVLPSPNVOSEWCHELYFAH 720
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 661 VPYLEKEDIOCLHERNFVPCKSIVENIINCIEKSYKISFVLPSPNVOSEWCHELYFAH 720
 XX
 Db 721 HNLFHFGSNNUJLILIPPIPNSTIPIKYHKAKLMORTIYQWPKEKSKGFLWANIRAA 780
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 721 HNLFHFGSNNUJLILIPPIPNSTIPIKYHKAKLMORTIYQWPKEKSKGFLWANIRAA 780
 XX
 Db 781 FNMKLTIVTENDVKS 796
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 781 FNMKLTIVTENDVKS 796
 XX
 RESULT 2
 ADP48601 ID 48601 standard; protein; 796 AA.
 XX AC ADP48601;
 XX DT 09-SEP-2004 (first entry)
 XX DE Human Toll-like receptor 6 protein SEQ ID NO:12.
 XX KW Toll-like receptor; TLR; human; detection; identification; TIR agonist;

KW TLR antagonist; Toll like receptor 6; TRL6; chromosome 4.
 XX OS Homo sapiens.
 XX PN WO2004053452-A2.
 XX PD 24-JUN-2004.
 XX FP 31-OCT-2003; 2003WO-US034554.
 XX PR 11-DEC-2002; 2002US-0432650P.
 XX DA (MINN) 3M INNOVATIVE PROPERTIES CO.
 XX PI Gupta SK, Ghosh TK, Fink JR;
 XX DR WPI; 2004-468955/44.
 XX N-PSDB; ADP48600.
 XX
 Detecting activation of Toll-like receptors (TLR) for identifying a TLR agonist or antagonist, comprises providing a cell culture comprising a reporter transfected with a sequence encoding a reporter. PS Claim 8; SEQ ID NO 12; 78P; English.
 XX
 The present invention describes a method for detecting activation of a Toll-like receptor (TLR) in a cell. The method comprises: (a) providing a cell culture comprising cells transfected with a nucleic acid sequence that encodes a reporter that (i) generates a detectable signal when the reporter is expressed and the cells are exposed to conditions for generating the detectable signal, and (ii) is operably linked to an expression control sequence that is induced by activation of a TLR and comprises a cytokine promoter, a chemokine promoter, a co-stimulatory marker promoter, or a defensin promoter; (b) exposing the cell culture to a compound that activates a TLR; (c) providing conditions for generating the detectable signal; and (d) detecting the detectable signal. Also described: (1) a method of identifying a TLR agonist or antagonist; (2) a pharmaceutical composition comprising a TLR agonist or antagonist identified by the method of (1) and a pharmaceutical salt. The methods are useful for detecting activation of a TLR in a cell and for identifying TLR agonist or antagonist. The present sequence represents a human TLR6 which is used in the exemplification of the present invention. The human TLR6 gene is located on chromosome 4, more specifically to 4p14. CC
 CC
 Sequence 796 AA:

Query Match 100.0%; Score 4154; DB 8; Length 796;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 796; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 MTKDKEPIVKSFHVCLMIIIVGTRIQFSDENEFAVDKSKEGLIHPKDLPLKTKVLDMS 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 1 MTKDKEPIVKSFHVCLMIIIVGTRIQFSDENEFAVDKSKEGLIHPKDLPLKTKVLDMS 60
 XX
 Db 61 QNYIAELQVSMSFSELTVRLSHRIQQLDSVFKFDLEYIDLSHNOLOKISCHPI 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 61 QNYIAELQVSMSFSELTVRLSHRIQQLDSVFKFDLEYIDLSHNOLOKISCHPI 120
 XX
 Db 121 USFRHDLDFNDFKALPICKFGNLSQNLFIGLSAMKLQKUDLPIAHHSYILDNR 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 121 USFRHDLDFNDFKALPICKFGNLSQNLFIGLSAMKLQKUDLPIAHHSYILDNR 180
 XX
 Db 181 YYIKENETESIQLINAKTILHIVFHPTSLFAIQNLQVNTGCOLTNIKUNDNNQVFIR 240
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 181 YYIKENETESIQLINAKTILHIVFHPTSLFAIQNLQVNTGCOLTNIKUNDNNQVFIR 240
 XX
 Db 241 FSELTRGLSTLNFTNHIEITWKCIVRVRVQFLPKPVENYIYLIESIREDDFTYS 300
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 241 FSELTRGLSTLNFTNHIEITWKCIVRVRVQFLPKPVENYIYLIESIREDDFTYS 300
 XX
 Db 301 KITLKALTIEHTNQVPLFSQTAIYVFSENMIMLITISDTPPIHLCPHAPSTKFPLN 360

|||||
301 KTTKALTIEHTINQVFLFSQALYTVFSENMIMLITISDTPFIMLCPHAPSTPKFLNF
360
361 TQNFVFDISIFERKSTVLKLETLIQLQNGLKDFKVGMLTKMPSLEILDWSNSLESGRH
420
361 TQNFVFDISIFERKSTVLKLETLIQLQNGLKDFKVGMLTKMPSLEILDWSNSLESGRH 420
Db
QY
421 KENCTWVESIIVLNLSNNMTDSVERCLPRTKVLDHSNKSVPKQVVKLEALQELNV 480
421 KENCTWVESIIVLNLSNNMTDSVERCLPRTKVLDHSNKSVPKQVVKLEALQELNV 480
QY
481 AFNSLTDLPGCGSFSSLSVLLIDHNVSHPRADEFFOSCOKRSIKAGDNPFQCTELREF 540
481 AFNSLTDLPGCGSFSSLSVLLIDHNVSHPRADEFFOSCOKRSIKAGDNPFQCTELREF 540
Db
QY
541 VRNIDQVSVSETLEGWDSDYKDYPESYRGSLDKDFMSELSCNTLIVIGATMLVAL 600
541 VRNIDQVSVSETLEGWDSDYKDYPESYRGSLDKDFMSELSCNTLIVIGATMLVAL 600
Db
QY
541 VRNIDQVSVSETLEGWDSDYKDYPESYRGSLDKDFMSELSCNTLIVIGATMLVAL 600
541 VRNIDQVSVSETLEGWDSDYKDYPESYRGSLDKDFMSELSCNTLIVIGATMLVAL 600
601 TVTSLCIVYLDPWYLRMWCOTQTRRARNPLQHAFISSEHDSAWKSEL 660
601 TVTSLCIVYLDPWYLRMWCOTQTRRARNPLQHAFISSEHDSAWKSEL 660
Db
QY
661 VPYLRKEDIOICLHERNFPVGRKSIVENINCIEKSYKSIVLSPNPNVOSIWCHYLYFAH 720
661 VPYLRKEDIOICLHERNFPVGRKSIVENINCIEKSYKSIVLSPNPNVOSIWCHYLYFAH 720
Db
QY
721 HNLFHGSNNLILIPPIONSIPNKHKALMTQTYLQWPKEKSKGLFWANIRAA 780
721 HNLFHGSNNLILIPPIONSIPNKHKALMTQTYLQWPKEKSKGLFWANIRAA 780
Db
QY
781 FMNKLTUVENDVKS 796
781 FMNKLTUVENDVKS 796
Db
RESULT 3
ADU23189
ID ADU23189 standard; protein: 796 AA.
XX
AC ADU23189;
XX
DT 27-JAN-2005 (first entry)
XX
DE Human Toll-like receptor 6 (TLR6) protein - SEQ ID 81.
XX
KW screening; Toll-like receptor agonist; TLR agonist; TLR6.
XX
OS Homo sapiens.
XX
PN WO2004094671-A2. /
XX
PD 04-NOV-2004.
XX
PF 22-APR-2004; 2004WO-US012788.
XX
PR 22-APR-2003; 2003US-0464586P.
XX
PR 22-APR-2003; 2003US-0464588P.
XX
PA (COLE-) COLEY PHARM GMBH.
PA (COLE-) COLEY PHARM GROUP INC.
XX
PT Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
DR MPI; 2004-795573/78.
XX
PT Identifying agonists of toll-like receptor (TLR) signaling activity,
PT useful therapeutically or prophylactically, comprises contacting an
PT RPM8226 cell that expresses a TLR with a test compound and measuring TLR
XX
PG Disclosure; SEQ ID NO 81; 342pp; English.

The invention comprises a screening method for identifying agonists of Toll-like receptor (TLR) signalling activity. The method involves contacting an RPM8226 cell (that expresses a TLR) with a test compound, and measuring a test level of TLR signalling activity, where a test level that is positive is indicative of a test compound that is a TIR agonist. The method of the invention is useful for identifying agonists of TLR. The present amino acid sequence represents a TLR protein.

Sequence 796 AA;

Query Match 100 %; Score 4154; DB 8; Length 796;
Best Local Similarity 100 %; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 796; Conservative 0; Mi smatches 0; Indels 0; Gaps 0;

Db 1 MTKDKEPPIVKSFPHYCMLIIVGTLIQFSQGNEFADVKSRKGLIITVPKDPLPKTVLDM 60
Db 1 MTKDKEPPIVKSFPHYCMLIIVGTRQFSDGNEFAVDKSKRGLIIVPKDPLPKTVLDM 60

QY 61 QNYIAQLQVSDMSFLSELSTVRLSNNRQQLDSVFKPNQDLEYDLSHNOLOKTSCHPI 120
Db 61 QNYIAQLQVSDMSFLSELSTVRLSNNRQQLDSVFKPNQDLEYDLSHNOLOKTSCHPI 120

Db 121 VSFRHDLDFNDKFALPICKEGFGNISOLNFIGLSAMKLQKUDLPTAHLHLSYILDRLN 180
Db 121 VSFRHDLDFNDKFALPICKEGFGNISOLNFIGLSAMKLQKUDLPTAHLHLSYILDRLN 180

QY 181 YYIKENETESESQILAKTTLHVEHPTSLF1QNSNTGCOLTNKUNDNCQFVK 240
Db 181 YYIKENETESESQILAKTTLHVEHPTSLF1QNSNTGCOLTNKUNDNCQFVK 240

QY 241 FLSELTRGSTLNFQNLHETWKLVRFQFLWKPVEVNTYLTIESIREDFTY 300
Db 241 FLSELTRGSTLNFQNLHETWKLVRFQFLWKPVEVNTYLTIESIREDFTY 300

QY 301 KTTKALTIEHTINQVFLFSQALYTVFSENMIMLITISDTPFIMLCPHAPSTPKFLNF 360
Db 301 KTTKALTIEHTINQVFLFSQALYTVFSENMIMLITISDTPFIMLCPHAPSTPKFLNF 360

QY 361 TQNFVFDISIFERKSTVLKLETLIQLQNGLKDFKVGMLTKMPSLEILDWSNSLESGRH 420
Db 361 TQNFVFDISIFERKSTVLKLETLIQLQNGLKDFKVGMLTKMPSLEILDWSNSLESGRH 420

QY 421 KENCTWVESIIVLNLSNNMTDSVERCLPRTKVLDHSNKSVPKQVVKLEALQELNV 480
Db 421 KENCTWVESIIVLNLSNNMTDSVERCLPRTKVLDHSNKSVPKQVVKLEALQELNV 480

QY 481 AFNSLTDLPGCGSFSSLSVLLIDHNVSHPRADEFFOSCOKRSIKAGDNPFQCTELREF 540
Db 481 AFNSLTDLPGCGSFSSLSVLLIDHNVSHPRADEFFOSCOKRSIKAGDNPFQCTELREF 540

QY 541 VRNIDQVSVSETLEGWDSDYKDYPESYRGSLDKDFMSELSCNTLIVIGATMLVAL 600
Db 541 VRNIDQVSVSETLEGWDSDYKDYPESYRGSLDKDFMSELSCNTLIVIGATMLVAL 600

QY 601 TVTSLCIVYLDPWYLRMWCOTQTRRARNPLQHAFISSEHDSAWKSEL 660
Db 601 TVTSLCIVYLDPWYLRMWCOTQTRRARNPLQHAFISSEHDSAWKSEL 660

QY 661 VPYLRKEDIOICLHERNFPVGRKSIVENINCIEKSYKSIVLSPNPNVOSIWCHYLYFAH 720
Db 661 VPYLRKEDIOICLHERNFPVGRKSIVENINCIEKSYKSIVLSPNPNVOSIWCHYLYFAH 720

QY 721 HNLFHGSNNLILIPPIONSIPNKHKALMTQTYLQWPKEKSKGLFWANIRAA 780
Db 721 HNLFHGSNNLILIPPIONSIPNKHKALMTQTYLQWPKEKSKGLFWANIRAA 780

QY 781 FMNKLTUVENDVKS 796
Db 781 FMNKLTUVENDVKS 796

ID	AAE16109 standard; Protein; 796 AA.	QY	121 VSFRHLDLSFNDKFALPKICKERGFLSQNENFLGLSAMKUDLPIAMHLSVILDRN 180
AC		Db	121 VSFRHLDLSFNDKFALPKICKERGFLSQNENFLGLSAMKUDLPIAMHLSVILDRN 180
XX		Db	
DT	26-MAR-2002 (first entry)	QY	181 YYIKENETESTLSQIQLNAKTHLVLFHPTSLFAIQNISVNWLGCQLTNKLNDNCQVFTR 240
XX		Db	181 YYIKENETESTLSQIQLNAKTHLVLFHPTSLFAIQNISVNWLGCQLTNKLNDNCQVFTR 240
KW	Human; DNAx Toll like receptor; DTLR; therapy; immunological disorder;	QY	241 FLSELTRGSTLNFTLNHETTWCILVRTOFLWPKPWFLYLNLYNTIESIRBEDFTYS 300
KW	interleukin 1; IL-1; screening; immunomodulator.	Db	241 FLSELTRGSTLNFTLNHETTWCILVRTOFLWPKPWFLYLNLYNTIESIRBEDFTYS 300
XX	Homo sapiens.	Db	
XX		Location/Qualifiers	
FH	Key	QY	301 KTKLKALTIIEHTINQVPLFSQTALEYTVSEMNIMMLTSIDTPFTHMLCPHAPSTPKELNF 360
FT	Peptide	Db	301 KTKLKALTIIEHTINQVPLFSQTALEYTVSEMNIMMLTSIDTPFTHMLCPHAPSTPKELNF 360
FT	/label= signal_peptide	Db	
FT	Protein	QY	361 TQNVFTDSIFEKCSTLVKEETLIQKNGKDKFLKGMLWIKMDMSLEIDWNSLESRRH 420
FT	32. .796	Db	361 TQNVFTDSIFEKCSTLVKEETLIQKNGKDKFLKGMLWIKMDMSLEIDWNSLESRRH 420
FT	Region	QY	421 KENCTIWVESTIVLNUSSNMNLTDSVFCRLPPRKVUDHANKIKSVPKQVKLEAQELAV 480
XX	549. .582	Db	421 KENCTIWVESTIVLNUSSNMNLTDSVFCRLPPRKVUDHANKIKSVPKQVKLEAQELAV 480
FT	/note= "Transmembrane segment"	Db	
XX	W0200190151-A2.	QY	481 AFNSLTDLPGCSFSSLVSLIDNSVSHPSADPQSQKOKRSIKAGDNPOQCTCELRF 540
PN	29-NOV-2001.	Db	481 AFNSLTDLPGCSFSSLVSLIDNSVSHPSADPQSQKOKRSIKAGDNPOQCTCELRF 540
XX	23-MAY-2001; 2001WO-US016766.	QY	541 VKNIQVSSVLELGMPDSYKCDYPSYRGSPLKOPFHMSELSNCNTLLITIGATMLVLA 600
XX	25-MAY-2000; 2000US-0207558P.	Db	541 VKNIQVSSVLELGMPDSYKCDYPSYRGSPLKOPFHMSELSNCNTLLITIGATMLVLA 600
PA	(SCHE) SCHERING CORP.	QY	601 TVTSCLVYLDPWYARMWCOTQTRRARNIPBLEQRNLQFHAFISSEHDSAWVSEL 660
PI	Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;	Db	601 TVTSCLVYLDPWYARMWCOTQTRRARNIPBLEQRNLQFHAFISSEHDSAWVSEL 660
XX		Db	
PT	WPI: 2002-083085/11.	QY	601 TVTSCLVYLDPWYARMWCOTQTRRARNIPBLEQRNLQFHAFISSEHDSAWVSEL 660
DR	N-PSDB; AAD26300.	Db	
XX		Db	
PT	New DNAx Toll like receptor (DTLR) proteins, useful for treating conditions exhibiting abnormal expression of the receptors of their ligands, particularly abnormalities manifested by immunological disorders.	QY	661 UPYLEKEPDQICLHERNFPVGKSIVENTINCIEKSYKSIVLSPNPFWOSEWCHVLYFAH 720
PT	Claim 1; Page 76; 297pp; English.	Db	661 UPYLEKEPDQICLHERNFPVGKSIVENTINCIEKSYKSIVLSPNPFWOSEWCHVLYFAH 720
XX		Db	
CC	The invention relates to mammalian receptor proteins, e.g., primate, human DNAx Toll like receptor (DTLR) protein and their corresponding nucleic acids. The DTLR is useful for treating conditions exhibiting abnormal expression of the receptors of their ligands. Such abnormality is manifested by immunological disorders. In particular, the DTLR is useful for treating various disease or disorders associated with abnormal expression or abnormal triggering of response to a ligand. The DTLR is also useful as an immunogen for the production of antisera or antibodies specific, e.g. capable of distinguishing between other interleukin (IL)-1 receptor family members, for the DTLR or its various fragments. The purified DTLR can be used to screen monoclonal antibodies or antigen-binding fragments. The antibodies are useful for screening expression libraries for particular expression products. These are useful for detecting or diagnosing various immunological conditions related to expression of DTLR or cells that express it. The present sequence is	QY	721 HNLFHEGSNLILIPPPONSPNPKYHKLAKMTQRTYIQLWPKEXKSIGRGLFWANIRAA 780
CC		Db	721 HNLFHEGSNLILIPPPONSPNPKYHKLAKMTQRTYIQLWPKEXKSIGRGLFWANIRAA 780
CC		Db	
CC		QY	781 FNMKLUTVENDVKS 796
CC		Db	781 FNMKLUTVENDVKS 796
CC		RESULT 5	
CC		ADU23188	
CC		ID	ADU23188 standard; protein; 796 AA.
CC		XX	
CC		AC	ADU23188;
CC		XX	
CC		DT	27-JAN-2005 (first entry)
CC		XX	
CC		DE	Human Toll-like receptor 6 (TLR6) protein - SEQ ID 80.
CC		XX	
CC		SQ	screening; Toll-like receptor agonist; TLR agonist; TLR6.
XX	Sequence 796 AA;	XX	
Query Match	99.9%; Score 4149; DB 5; Length 796;	OS	
Best Local Similarity	99.9%; Pred. No. 0;	XX	
Matches	795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	XX	
OY		XX	
1	MTKDKPEPKVPHFVCMITVGTROPSDGEFAVAKSKRQLHLVPKDLPLKTYLDM 60	XX	
1	MTKDKPEPKVPHFVCMITVGTROPSDGEFAVAKSKRQLHLVPKDLPLKTYLDM 60	XX	
Db		XX	
OY	61 QNYIAELQVSMSPLSLETVLRLSHRIQLDLSVFKENQDOLYDLSHNOLOQKISCHPI 120	XX	
61 QNYIAELQVSMSPLSLETVLRLSHRIQLDLSVFKENQDOLYDLSHNOLOQKISCHPI 120	XX		
Db		XX	

PA (COLE-) COLEY PHARM GMBH.
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
 XX DR WPI; 2004-795573/78.

PT Identifying agonists of toll-like receptor (TLR) signaling activity,
 PT useful therapeutically or prophylactically, comprises contacting an
 PT RPL8226 cell that expresses a TLR with a test compound and measuring TLR
 PT signaling activity.

XX Disclosure; SEQ ID NO 80; 342pp; English.

XX The invention comprises a screening method for identifying agonists of
 CC toll-like receptor (TLR) signalling activity. The method involves
 CC contacting an RPL8226 cell (that expresses a TLR) with a test compound,
 and measuring a test level of TLR signalling activity, where a test level
 CC that is positive is indicative of a test compound that is a TLR agonist.
 CC The method of the invention is useful for identifying agonists of TLR.
 CC The present amino acid sequence represents a TLR protein.

XX Sequence 796 AA;

Query Match	99.9%	Score 4149;	DB 8;	Length 796;
Best Local Similarity	99.9%	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 795;	Conservative 0;	Gaps 0;		

QY 1 MTKDKERPIVKSFHFCVCLMIVGTRIQPSDGNEFAVDKSKKGHLIRPKDPLKTKLDM 60
 Db 1 MTKDKERPIVKSFHFCVCLMIVGTRIQPSDGNEFAVDKSKKGHLIRPKDPLKTKLDM 60
 QY 61 QNYIAELQVSMSFLSLETVRLSHNRIQLDLSVRFKNQDLEYDLSHNOLOKISCHPI 120
 Db 61 QNYIAELQVSMSFLSLETVRLSHNRIQLDLSVRFKNQDLEYDLSHNOLOKISCHPI 120
 QY 121 VSFRHLDLSFNDPKALPICKERFGNLSQNLFLGLSAMLQKDLPPLAHLHSYILDRN 180
 Db 121 VSFRHLDLSFNDPKALPICKERFGNLSQNLFLGLSAMLQKDLPPLAHLHSYILDRN 180
 QY 181 YYKIKENETESTQILNAKTHLHFPHPTSLFATQVNISTLQQLTNIKLDNCQFIK 240
 Db 181 YYKIKENETESTQILNAKTHLHFPHPTSLFATQVNISTLQQLTNIKLDNCQFIK 240
 QY 241 PSELUTRGSTLQFTNFTNHIEFTWKCLVRFQDLPKVEVNLINYNTIESREEPFTS 300
 Db 241 PSELUTRGSTLQFTNFTNHIEFTWKCLVRFQDLPKVEVNLINYNTIESREEPFTS 300
 PS 301 KTYTKALKTIEHTTNQVLFLSPOTALYTWFSEMMILMTSDTPFTHMLCPHAPSTFKLNF 360
 Db 301 KTYTKALKTIEHTTNQVLFLSPOTALYTWFSEMMILMTSDTPFTHMLCPHAPSTFKLNF 360
 QY 361 TQNFVTDISIFEKCSLTLKLTULQOKGLDFKVGMKTQMPKSLBDLVWSNSLGRH 420
 Db 361 TQNFVTDISIFEKCSLTLKLTULQOKGLDFKVGMKTQMPKSLBDLVWSNSLGRH 420
 QY 421 KENCTWESIWTNLSSNMLDSVRCLLPRKYLKDLHSNKSKVPRQVWKEALQBINV 480
 Db 421 KENCTWESIWTNLSSNMLDSVRCLLPRKYLKDLHSNKSKVPRQVWKEALQBINV 480
 QY 481 AFNSLTDLPGCFSFSSLVLDHNSVHPADFFGSCQKQRSIKAGDNPPQCTCELF 540
 Db 481 AFNSLTDLPGCFSFSSLVLDHNSVHPADFFGSCQKQRSIKAGDNPPQCTCELF 540
 QY 541 VKNIDOVSEVNGWPDSYKCPYSESRSPLKDFRMSSELSENITLIVTGATMLVAV 600
 Db 541 VKNIDOVSEVNGWPDSYKCPYSESRSPLKDFRMSSELSENITLIVTGATMLVAV 600
 QY 601 TVTSLCYLDDFLWYRLRMWCQWOTRRAPIRNLQHAFSYSESDSAWTKEL 660
 Db 601 TVTSLCYLDDFLWYRLRMWCQWOTRRAPIRNLQHAFSYSESDSAWTKEL 660
 QY 661 VPYLEKEDIQICLHERNPVPGKGSIVENINCIEKSYKSIFVLSPNFVQSEWCHYLYFAH 720

Db 661 VPYLEKEDIQICLHERNPVPGKGSIVENINCIEKSYKSIFVLSPNFVQSEWCHYLYFAH 720
 ID ADU23190 standard; protein; 796 AA.
 KX
 AC ADU23190;
 DT 27-JAN-2005 (first entry)
 XX Human Toll-like receptor 6 (TLR6) protein - SEQ ID 82.
 DE screening; Toll-like receptor agonist; TLR agonist; TLR6.
 XX RESULT 6
 OS Homo sapiens.
 XX WO2004094671-A2.
 XX PD 04-NOV-2004.
 XX PF 22-APR-2004; 2004WO-US012788.
 XX PR 22-APR-2003; 2003US-0464586P.
 PR 22-APR-2003; 2003US-0464588P.
 XX PA (COLE-) COLEY PHARM GMBH.
 PA (COLE-) COLEY PHARM GROUP INC.
 XX PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
 XX DR WPI; 2004-795573/78.
 PT Identifying agonists of toll-like receptor (TLR) signalling activity,
 PT useful therapeutically or prophylactically, comprises contacting an
 PT RPL8226 cell that expresses a TLR with a test compound and measuring TLR
 PT signalling activity.

XX Disclosure; SEQ ID NO 82; 342pp; English.

XX The invention comprises a screening method for identifying agonists of
 CC toll-like receptor (TLR) signalling activity. The method involves
 CC contacting an RPL8226 cell (that expresses a TLR) with a test compound,
 and measuring a test level of TLR signalling activity, where a test level
 CC that is positive is indicative of a test compound that is a TLR agonist.
 CC The method of the invention is useful for identifying agonists of TLR.
 CC The present amino acid sequence represents a TLR protein.

XX Sequence 796 AA;

Query Match	99.9%	Score 4149;	DB 8;	Length 796;
Best Local Similarity	99.9%	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 795;	Conservative 0;	Gaps 0;		

QY 1 MTKDKERPIVKSFHFCVCLMIVGTRIQPSDGNEFAVDKSKKGHLIRPKDPLKTKLDM 60
 Db 1 MTKDKERPIVKSFHFCVCLMIVGTRIQPSDGNEFAVDKSKKGHLIRPKDPLKTKLDM 60
 QY 61 QNYIAELQVSMSFLSLETVRLSHNRIQLDLSVRFKNQDLEYDLSHNOLOKISCHPI 120
 Db 61 QNYIAELQVSMSFLSLETVRLSHNRIQLDLSVRFKNQDLEYDLSHNOLOKISCHPI 120
 QY 121 VSFRHLDLSFNDPKALPICKERFGNLSQNLFLGLSAMLQKDLPPLAHLHSYILDRN 180

DR	DR	DR	
N-PSDB;	ADX06215.		
PT	Biomarkers useful for predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclin-dependent kinase activity.		
PT	to a cancer treatment comprising administration of a modulator of cyclin-dependent kinase activity.		
XX	Claim 5; SEQ ID NO 781; 141pp; English.		
CC	This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-responsing agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:12456 EST W8729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers.		
CC	The cdk modulator is preferably N-(5-[15-(1,1-Dimethyltetrahydro-2-oxazolyl)methylthio]-2-thiazolyl-4-piperidine carbonyl amide, 0.5-1-tartaric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/int/patent/seqdb. This sequence represents a biomarker used in the method of the invention.		
CC	part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/int/patent/seqdb. This sequence represents a biomarker used in the method of the invention.		
CC	Sequence 796 AA;		
CC	Query Match		
CC	Best Local Similarity	99.9%	
CC	Matches	975;	
CC	Conservative	0;	
CC	Mismatches	0;	
CC	Gaps	0;	
CC	Indels	1;	
Qy	1		
Db	WTKDKDEPIVKVSHFHVCLMIIITIVGTRIQFSDENEFAVDKSKRGLIHVKDPLPKTVLMS	60	
Qy	61	QWYIAELQVSNSMFLSBLTIVRLSHNRIOQLDLSVFKENQDIEYLDISHNQLOKISCHPI	120
Db	61	QWYIAELQVSNSMFLSBLTIVRLSHNRIOQLDLSVFKENQDIEYLDISHNQLOKISCHPI	120
Qy	121	VSRHDLISFDKFALPICKEGNLSONLNFGLISAMKQDLPDTAHLHSYILDRN	180
Db	121	VSRHDLISFDKFALPICKEGNLSONLNFGLISAMKQDLPDTAHLHSYILDRN	180
Qy	181	VYKENETESTQLNAKTLHVHPPLSLFAQVNISNTLGLQMTKLNDNCQFIK	240
Db	181	VYKENETESTQLNAKTLHVHPPLSLFAQVNISNTLGLQMTKLNDNCQFIK	240
Qy	241	FSELTRGSTLNFTNHIEITWKCLVRVFPQFLWPKVEVYIYNLTIESIREDDFTY	300
Db	241	FSELTRGSTLNFTNHIEITWKCLVRVFPQFLWPKVEVYIYNLTIESIREDDFTY	300
Qy	301	KTTKALTIEHTINQVFLSOTALYTIVFSEMINIMULTISDTPRTHMCPHASTFKLFN	360
Db	301	KTTKALTIEHTINQVFLSOTALYTIVFSEMINIMULTISDTPRTHMCPHASTFKLFN	360
Qy	361	TQNFUDSIFEKCSTLVKLETLIQLQNLKDFLKVGMLTKMPSLELDVSNLSLESGRH	420
Db	361	TQNFUDSIFEKCSTLVKLETLIQLQNLKDFLKVGMLTKMPSLELDVSNLSLESGRH	420
Qy	421	KENCTWESIVVLNLSSNMLTDSPVRCPLPRKVLDLHSNKISKVPQVKWALEQBNV	480
Db	421	KENCTWESIVVLNLSSNMLTDSPVRCPLPRKVLDLHSNKISKVPQVKWALEQBNV	480
Qy	481	AFNSLTDLGCGSFSSLVLLIDHNSVSHPSADFFSCQKSIKAGDNFOCTCEREF	540
Db	481	AFNSLTDLGCGSFSSLVLLIDHNSVSHPSADFFSCQKSIKAGDNFOCTCEREF	540
Qy	541	VNIDQNSSEVLEGWPDSYKDYPEYRGSLKDFHMSCLNITLIVGTMVLAV	600
Db	541	VNIDQNSSEVLEGWPDSYKDYPEYRGSLKDFHMSCLNITLIVGTMVLAV	600
XX	RESULT 7		
XX	ID ADX06216		
XX	ID ADX06216 standard; protein; 796 AA.		
XX	AC ADX06216;		
XX	DT 21-APR-2005 (first entry)		
XX	DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 781.		
XX	XX cytostatic; cyclin-dependent kinase; cdk; biomarker.		
XX	OS Homo sapiens.		
XX	PN WO2005012873-A2.		
XX	PR 29-JUL-2003; 2003US-0490890P.		
XX	PD 10-FEB-2005.		
XX	PP 29-JUL-2004; 2004WO-US024424.		
XX	PA (BRIM) BRISTOL-MYERS SQUIBB CO.		
XX	PI Li M., Rupnow BA, Webster KR, Jackson DG, Wong TW;		

Db	541 VKNIDQSVSEVLEGWGPDSYKCDYPESTRGSPLKDFHNSELSCNITLIVTGMVLAV	600	Db	61 QNYIAELQVSQMSFLBETVRLSHNRQLLDLSVFRNQDLEYLDSHNLQQLQKTSCHPI	120
Qy	601 TVSLCIVLDLPLWYLRMVCQWTRRARNPLFELORNQLOHAFTSYSEHSDSAWVSEL	660	Qy	121 VSFRHDLFSNDPKALPICKERGNLSQUNFLGSLSAMNQKQUDLPFLAHLSYIILDRN	180
Db	601 TVSLCIVLDLPLWYLRMVCQWTRRARNPLFELORNQLOHAFTSYSEHSDSAWVSEL	660	Db	121 VSFRHDLFSNDPKALPICKERGNLSQUNFLGSLSAMNQKQUDLPFLAHLSYIILDRN	180
Qy	661 VVYLEKEDIQICLHERNFPVPGKSIVENINCIEKSYKSFIVLSPNFTQSEWCHYELFAH	720	Qy	181 YTKENESTESLOQINAKTHLYVPHPTSLAFQVNISNTLGCLQLTNIKLANDNCQFIK	240
Db	661 VVYLEKEDIQICLHERNFPVPGKSIVENINCIEKSYKSFIVLSPNFTQSEWCHYELFAH	720	Db	181 YTKENESTESLOQINAKTHLYVPHPTSLAFQVNISNTLGCLQLTNIKLANDNCQFIK	240
Qy	721 HNLFHEGSNNLILLIPONSIIPNKHKUKALMTQRTYLOWPKESKRGFLFWANIRAA	780	Qy	241 FISELTGGSTLNFTNLHETWMKCLRVFQTLWPKVYLMYLNLTIESREDEPTYS	300
Db	721 HNLFHEGSNNLILLIPONSIIPNKHKUKALMTQRTYLOWPKESKRGFLFWANIRAA	780	Db	241 FLSLBTHGPTLNFNTLHETWMKCLRVFQTLWPKVYLMYLNLTIESREDEPTYS	300
Qy	781 FNMKLTUVTENDVKS 796		Qy	301 KTKKALTIETHTNQVLFQSLALYTSEMMUTISDPFPIMCPHAPSTFKELNF	360
Db	781 FNMKLTUVTENDVKS 796		Db	301 KTKKALTIETHTNQVLFQSLALYTSEMMUTISDPFPIMCPHAPSTFKELNF	360
RESULT 8			Qy	361 TQVFVTSIFEKCSITVLUKLETLLQNGKLDFKVGATKOMPSETLTDVWSNSLESGRH	420
ID	AYY8054	standard; protein; 796 AA.	Db	361 TQVFVTSIFEKCSITVLUKLETLLQNGKLDFKVGATKOMPSETLTDVWSNSLESGRH	420
XX			Qy	421 KENCTWVESTIVVNLSSNMLTDSVFRCLPPRKVLDLHSNKTSKVPRQVKVLEALQRBNV	480
AC	AYY8054;		Db	421 KENCTWVESTIVVNLSSNMLTDSVFRCLPPRKVLDLHSNKTSKVPRQVKVLEALQRBNV	480
XX			Qy	481 ATNSLTDLPGCSSSISVLIHDNSHSPADPQSQKRSIKAGDNPQCTSELR	540
DT	22-SEP-2000. (first entry)		Db	481 ATNSLTDLPGCSSSISVLIHDNSHSPADPQSQKRSIKAGDNPQCTSELR	540
DE	Human Toll-like receptor TLR6 protein.		Qy	541 VKNIDQSVSEVLEGWGPDSYKCDYPESTRGSPLKDFHNSELSCNITLIVTGMVLAV	600
XX			Db	541 VKNIDQSVSEVLEGWGPDSYKCDYPESTRGSPLKDFHNSELSCNITLIVTGMVLAV	600
KW	Toll-like receptor; TLR6; human; antiinfectious; treatment; infection;		Qy	601 TVSLCIVLDLPLWYLRMVCQWTRRARNPLFELORNQLOHAFTSYSEHSDSAWVSEL	660
TM	transcription factor; NF-kappaB; immune response.		Db	601 TVSLCIVLDLPLWYLRMVCQWTRRARNPLFELORNQLOHAFTSYSEHSDSAWVSEL	660
OS	Homo sapiens.		Qy	661 VVYLEKEDIQICLHERNFPVPGKSIVENINCIEKSYKSFIVLSPNFTQSEWCHYELFAH	720
XX			Db	661 VVYLEKEDIQICLHERNFPVPGKSIVENINCIEKSYKSFIVLSPNFTQSEWCHYELFAH	720
PN	WO200024776-A1.		Qy	721 HNLFHEGSNNLILLIPONSIIPNKHKUKALMTQRTYLOWPKESKRGFLFWANIRAA	780
PD	04-MAY-2000.		Db	721 HNLFHEGSNNLILLIPONSIIPNKHKUKALMTQRTYLOWPKESKRGFLFWANIRAA	780
XX			Qy	781 FNMKLTUVTENDVKS 796	
PP	26-OCT-1999; 99WO-JP005917.		Db	781 FNMKLTUVTENDVKS 796	
XX			Qy		
PR	26-OCT-1998; 98JP-00304110.		Db		
PA	(NISCC-) JAPAN SCI & TECHNOLOGY CORP.		Qy		
XX			Db		
PA	Pt Akira S, Takeuchi O;		Qy		
XX			Db		
DR	WPI; 2000-350697/30.		Qy		
DR	N-PSDB; AIA39809.		Db		
XX			Qy		
PT	Toll-like receptor TLR6 molecule and encoded gene, participating in signal transduction of initial immune response, applicable e.g. in treating infections.		Db		
PS	Claim 1; Page 27-29; 35PP; Japanese.		Qy		
XX			Db		
CC	This invention describes a novel toll-like receptor TLR6 which has antiinfectious activity. The protein and its encoded gene have clinical use e.g. in treating infections. Toll family receptors are related to transcription factor NF-kappaB and regulate the expression of various genes participating in the immune response. This sequence represents the human TLR6 protein which is described in the method of the invention		Qy		
SQ	Sequence 796 AA;		Db		
RESULT 9			Qy		
ID	AEE16112	standard; protein; 780 AA.	Db		
XX			Qy		
AC	AEE16112;		Db		
XX			Qy		
DT	26-MAR-2002 (first entry)		Db		
DE	Human DNAx Toll like receptor (DTLR) 9 #2, alternative version.		Qy		
XX			Db		
KW	Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder; interleukin 1; IL-1; screening; immunomodulator.		Qy		
XX			Db		
OS	Homo sapiens.		Qy		
Key Location/Qualifiers			Db		
FF	Peptide	Location/Qualifiers	Qy		
FT	/label= Signal_peptide	Location/Qualifiers	Db		
FT	Protein	Location/Qualifiers	Qy		
FT	/note= "Human mature DTLR9"	Location/Qualifiers	Db		
FT	Misc-difference 176. .177	Location/Qualifiers	Qy		
Matches			Db		
1	MTDKDEPIVKSRHFCVMIITVGRQFSDGNFBAVKSKRGLIHVRKDPLIKTVLDM	60	Qy		
1	MTDKDEPIVKSRHFCVMIITVGRQFSDGNFBAVKSKRGLIHVRKDPLIKTVLDM	60	Db		
61	QNYIAELQVSQMSFLBETVRLSHNRQLLDLSVFRNQDLEYLDSHNLQQLQKTSCHPI	120	Qy		
61	QNYIAELQVSQMSFLBETVRLSHNRQLLDLSVFRNQDLEYLDSHNLQQLQKTSCHPI	120	Db		

FT /note= "Encoded by CTGGATTAGAACTTATTATATAAGAA
 FT ATTCGACGAACTCTAACATT"
 FT Region 549 .582
 FT /note= "Transmembrane segment"
 XX
 PN WO200190151-A2.
 XX
 PD 29-NOV-2001.
 XX
 PR 23-MAY-2001; 2001WO-US016766.
 XX
 PR 25-MAY-2000; 2000US-0207558P.
 XX
 PA (SCH) SCHERRING CORP.
 XX
 PI Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
 XX
 DR WPI; 2002-083085/11.
 XX
 N-PSB; AAD26300.
 XX
 PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, Particularly abnormalities manifested by immunological
 PT disorders.
 XX
 PS Claim 1; Page 274-276; 297pp; English.
 XX
 CC The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DNAX Toll like receptor (DTLR) protein and their corresponding
 CC nucleic acids. The DTLR is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTLR is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTLR is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTLR or its various fragments. The
 CC purified DTLR can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression
 CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC human DTLR or cells that express it. The present sequence is
 CC ID NO 41 is stated to be similar to the sequence shown in page 76
 CC (AAE16109). However these sequences differ at several locations
 XX
 SQ Sequence 780 AA;

Query Match 97.4%; Score 4048; DB 5; Length 780;
 Best Local Similarity 97.9%; Pct. No. 0; Mismatches 1; Indels 16; Gaps 1;
 Matches 779; Conservative 0; Pairs 0; Gaps 0.

Qy 1 MTKDKEPIVKPHFVCLMIIIVGTRQFSDENEPAVDKSKGKLIHVKDPLIKTKLDM 60
 Db 1 MTKDKEPIVKPHFVCLMIIIVGTRQFSDENEPAVDKSKGKLIHVKDPLIKTKLDM 60
 Qy 61 QNYIAELQVSMSFLSFLDPTVRLSHRIQLQDLSVRFNQLEYVLDHSNQLOKISCHPI 120
 Db 61 QNYIAELQVSMSFLSFLDPTVRLSHRIQLQDLSVRFNQLEYVLDHSNQLOKISCHPI 120
 Qy 121 VSFRHDLDFNDPKALPICKEGFNGNLSONFLNFGISAMKLQDLPFAHLHSLYILLDRN 180
 Db 121 VSFRHDLDFNDPKALPICKEGFNGNLSONFLNFGISAMKLQDLPFAHLHSLYILL--- 176
 Qy 181 YYIKENETESLQINAKTLPHYFHPFLAFQVNISINTLGQLQNIKNDNCQVFIK 240
 Db 177 -----TNAKTHLHVPHPTSLFLAFIGVNISNTLGQLQNIKNDNCQVFIK 224
 Qy 241 FUSELTGRGSTLNFNTLHIEITWKCLVRVQFLWPKVEYLNLYNLTIESREEDFTYS 300
 Db 225 FISELARGPTLNFNTLHIEITWKCLVRVQFLWPKVEYLNLYNLTIESREEDFTYS 284
 XX
 301 KITLKALTIEHTNQVFLFSQTALEYVFSEMINMMLTSIDTPFHMLCPHAPSTFKFLNP 360

Db 285 KTIKLALTIEHTNQVFLFSQTALEYVFSEMINMMLTSIDTPFHMLCPHAPSTFKFLNF 344
 Qy 361 TONVFDISFEKCSPLVKLEPLIQKNGLKDLFKVGLMTKDMPSLIEDLDSWNSLDEGRH 420
 Db 345 TONVFDISFEKCSPLVKLEPLIQKNGLKDLFKVGLMTKDMPSLIEDLDSWNSLDEGRH 404
 Qy 421 KENCTWESIWLNLSSNMLTDSPVRCPLPRKVLDHSNKKSVPKQVVKLEALQELAV 480
 Db 405 KENCTWESIWLNLSSNMLTDSPVRCPLPRKVLDHSNKKSVPKQVVKLEALQELAV 464
 Qy 481 AFNSLTDLPGGSFSSLVSLIDHSVSHSADFFQSQDORSIKAGDNFOCTCLREF 540
 Db 465 AFNSLTDLPGGSFSSLVSLIDHSVSHSADFFQSQDORSIKAGDNFOCTCLREF 524
 Qy 541 VRNIDOVSEVTELEGWNDSYKCDYPSEYRSPLKDFHMSELSCNTLILIVTGATMLAV 600
 Db 525 VRNIDOVSEVTELEGWDPSYKCDYPSEYRSPLKDFHMSELSCNTLILIVTGATMLAV 584
 Qy 601 TVTSICLYLDPWLMCOTQRRAARNPLERLQRNLQPHAFISSEHDSSAWKSEL 660
 Db 585 TVTSICLYLDPWLMCOTQRRAARNPLERLQRNLQPHAFISSEHDSSAWKSEL 644
 Qy 661 UPYLEKEDIQICLHERNFWVGKSVTENNINGEKSYSKIFVLSPENFVQSWCHBLEYFAH 720
 Db 645 UPYLEKEDIQICLHERNFWVGKSVTENNINGEKSYSKIFVLSPENFVQSWCHBLEYFAH 704
 Qy 721 HNLFHFGGSNNLITTLEPIFONSPIRNKYKUKALMORTYIOWPKEKSKERGLFWANIRAA 780
 Db 705 HNLFHFGGSNNLITTLEPIFONSPIRNKYKUKALMORTYIOWPKEKSKERGLFWANIRAA 764
 Qy 781 FNMKLTIVTENNDVK 796
 Db 765 FNMKLTIVTENNDVK 780
 DT RESULT 10
 ID AAU25469
 ID AAU25469 standard; protein; 781 AA.
 XX
 AC AAU25469;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human mddt protein from clone LI:007302.1:2000MAY01.
 XX
 Human; molecules for disease detection and treatment; mddt;
 KW Human; molecules for disease detection and treatment; mddt;
 KW Antiarteriosclerotic; hepatotropic; cytostatic;
 KW immunosuppressive; antidiabetic; antiasthmatic; neuroprotective;
 KW osteopathic; antiarrhythmic; cell proliferative disorder;
 KW arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma;
 KW leukemia; breast cancer; autoimmune disorder; AIDS;
 KW acquired immunodeficiency syndrome; Addison's disease; diabetes mellitus;
 KW asthma; multiple sclerosis; osteoarthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200162922-A2.
 XX
 PD 30-AUG-2001.
 XX
 PR 21-FEB-2001; 2001WO-US005989.
 XX
 PR 24-FEB-2000; 2000US-0185213P.
 PR 16-MAY-2000; 2000US-0205232P.
 PR 17-MAR-2000; 2000US-0205285P.
 PR 17-MAY-2000; 2000US-0205286P.
 PR 17-MAY-2000; 2000US-0205287P.
 PR 17-MAY-2000; 2000US-0205233P.
 PR 17-MAY-2000; 2000US-0205324P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX

PI Panzer SR, Spiro PA, Banville SC, Shah P, Chaloup MS, Chang SC;
 PI Chen A, D' Sa S, Amshay S, Dahl CR, Dam TC, Daniels SE, Dufour GE;
 PI Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL, Liu TF;
 PI Roseberry AM, Rosen BH, Russo FD, Stockdrehner MK, Daffo A;
 PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W;
 PI Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;

XX XX WPI; 2001-570631/64.

DR DR N-PSDB; AAS42521.

PT PT New disease detection and treatment molecule poly nucleotides and
 PT cirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mellitus,
 PT asthma and multiple sclerosis.

XX XX Claim 27; Page 180-182, 183pp; English.

CC CC The invention relates to novel human molecules for disease detection and
 treatment (mdt proteins) and the poly nucleotides encoding them. The MDT
 CC poly nucleotides and polypeptides are useful for diagnostic and
 therapeutic purposes e.g. to diagnose and treat cell proliferative
 CC disorders (e.g. arteriosclerosis, cirrhosis and psoriasis), cancers (e.g.
 adenocarcinoma, leukaemia and breast cancer) autoimmune disorders (e.g.
 CC acquired immunodeficiency syndrome (AIDS) and Adinson's disease) diabetes
 CC mellitus, asthma, multiple sclerosis, osteoarthritis, and many more
 CC diseases given in the specification. The present sequence represents an
 mdt protein of the invention

XX XX Sequence '781 AA;

Query Match 96.8%; Score 4021; DB 4; Length 781;
 Best Local Similarity 99.9%; Pred. No. 0; Gaps 0;
 Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTKDKERPIVKSFHFVCLMILIVGTRIQFSDNEFAVDKSKGKGLIHPKDPLKTKVLDMS 60
 Db 7 MTKDKERPIVKSFHFVCLMILIVGTRIQFSDNEFAVDKSKGKGLIHPKDPLKTKVLDMS 66
 Qy 61 ONYIAELQVSMSFLSBLTIVRLSHRNQLDLSVFKNQLEYDLSHNGNQLQKISCHPI 120
 Db 67 ONYIAELQVSMSFLSBLTIVRLSHRNQLDLSVFKNQLEYDLSHNGNQLQKISCHPI 126
 Qy 121 VSFRHDLDFMDPKALPICKERFGNLSQLNFGQLSAMKLQKDLPKHLHSYILDNR 180
 Db 127 VSFRHDLDFNDPKALPICKERFGNLSQLNFGQLSAMKLQKDLPKHLHSYILDNR 186
 Qy 181 YYIKENETESTQILNAKTLHVFHPTSLFAIQVNISNTYCLQLTNKNDNCQFVK 240
 Db 187 YYIKENETESTQILNAKTLHVFHPTSLFAIQVNISNTYCLQLTNKNDNCQFVK 246
 Qy 241 FLSELTRGSTLNFNLTHNIEFTWKCLVRVFLWPKPEVYNIYNTIESIREEDFTY 300
 Db 247 FLSELTRGSTLNFNLTHNIEFTWKCLVRVFLWPKPEVYNIYNTIESIREEDFTY 306
 Qy 301 KTKLKLALTIBHITNQFLPFSQTALYWFSSENAMIMMTISDTPFIRMLCPHAPSTKPLNF 360
 Db 307 KTKLKLALTIBHITNQFLPFSQTALYWFSSENAMIMMTISDTPFIRMLCPHAPSTKPLNF 366
 Qy 361 TQNVFTDSIFFKCSIKVKELETLQKNGKLDFKVSLMTKOMPSLFLDVSNSLESGRH 420
 Db 367 TQNVFTDSIFFKCSIKVKELETLQKNGKLDFKVSLMTKOMPSLFLDVSNSLESGRH 426
 Qy 421 KENCTWVESTVNLNSNNMLTDVSFLCPLPPRKVUDLHSNKKSVKQVYLAQELNV 480
 Db 427 KENCTWVESTVNLNSNNMLTDVSFLCPLPPRKVUDLHSNKKSVKQVYLAQELNV 486
 Qy 481 AFNSLTDLPGGSFSSLVLTIDHNVSHPADFFOSCQKRSIKAGDNPFQCTBREF 540
 Db 487 AFNSLTDLPGGSFSSLVLTIDHNVSHPADFFOSCQKRSIKAGDNPFQCTBREF 546
 Qy 541 VKNIDQVSSELEGWDSYKDYPESYRGSLKDPMSELSCNITLIVGATMVLAV 600
 Db 547 VKNIDQVSSELEGWPSYKDYPESYRGSPLKDFMSLSCNITLIVGATMVLAV 606

RESULT 11
 ID ADU23197 standard; protein; 795 AA.
 XX XX AC ADU23197;
 XX XX DT 27-JAN-2005 (first entry)
 XX XX DE Murine Toll-like receptor 6 (TLR6) protein - SEQ ID 89.
 XX XX KW screening; Toll-like receptor agonist; TLR agonist; TLR6.
 XX XX OS Mus sp.
 XX XX PN WO2004094671-A2.
 XX XX PD 04-NOV-2004.
 XX XX PF 22-APR-2004; 2004WO-US012788.
 PR 22-APR-2003; 2003US-0464586P.
 PR 22-APR-2003; 2003US-0464588P.
 XX XX PA (COLE-) COLEY PHARM GMBH.
 PA (COLE-) COLEY PHARM GROUP INC.
 XX PT Vollmer J, Jurek M, Lipford GB, Schetter C, Forzbach A, Krieg AM;
 XX DR WPI; 2004-795573/78.
 XX PT Identifying agonists of toll-like receptor (TLR) signaling activity,
 PT useful therapeutically or prophylactically, comprises contacting an
 PT RPMI226 cell that expresses a TLR with a test compound and measuring TLR
 PT signaling activity.
 XX DS Disclosure; SEQ ID NO 89; 342pp; English.
 XX DS The invention comprises a screening method for identifying agonists of
 CC Toll-like receptor (TLR) signalling activity. The method involves
 CC contacting an RPMI226 cell (that expresses a TLR) with a test compound,
 CC and measuring a test level of TLR signalling activity, where a test level
 CC that is positive is indicative of a test compound that is a TLR agonist.
 CC The method of the invention is useful for identifying agonists of TLR.
 CC The present amino acid sequence represents a TLR protein.

XX XX Sequence '795 AA;

Query Match 75.7%; Score 3144.5; DB 8; Length 795;
 Best Local Similarity 79.9%; Pred. No. 3.9e-254;
 Matches 588; Conservative 97; Mismatches 110; Indels 1; Gaps 1;

Qy 1 MTKDKERPIVKSFHFVCLMILIVGTRIQFSDNEFAVDKSKGKGLIHPKDPLKTKVLDMS 60
 Db 1 MSQDRKFPIVSSFHFCALALIVGSMTPFSNBSLESMDYSRNLLHVPKDPLKTKVLDMS 60
 Qy 61 ONYIAELQVSMSFLSBLTIVRLSHRNQLDLSVFKNQLEYDLSHNGNQLQKISCHPI 120
 Db 61 QNSISBLRMPDIFSLERVRLSHRNRLSIDFHTFLPQDLEYDLSHNGNQLQKISCHPI 120

QY 121 VSFRHLDLSNDPKALPICKERFGNISQNLNGLSAMKLOQKLPIAHHSYILDAN 180
PA (COLE-) COLEY PHARM GROUP INC.
DB 121 ASLRHLDLSNDFDYLPUCKEFGNLTKLFLGSLAKFRQDLPVALVHLSCILDLVS 180 XX
XX PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
XX DR WPI; 2004-795573/78.

QY 181 YYIKENETESTIQIQLNAKTLHWFHTSLFAMIQNISVNTGCOLTNKLANDNCQVFIR 240
DB 181 YYIKGGETESIQIQLNAKTLHWFHTSLFAMIQNISVNTGCOLTNKLANDNCQVFIR 240 PT identifying agonists of Toll-like receptor (TLR) signaling activity,
PT useful therapeutically or prophylactically, comprises contacting an
PT RPM8226 cell that expresses a TIR with a test compound and measuring TIR
PT signalling activity.

QY 241 FLSELTRGSTLNFNTHIETWKCIVRUFQFLWPKPVEYNTNTITESIREDFTYS 300 XX
DB 241 FLSELTRGSTLNFNTHIETWKCIVRUFQFLWPKPVEYNTNTITESIREDFTYS 300 PS Disclosure; SEQ ID NO 87; 34pp; English.

QY 301 KITLKALTIETINQFLSQTAUYTFSENIMMLTISDTPFIMLCRPASTEKFLENF 360 XX
DB 301 ETALKSMLIEHVKNQYFLSKPEALYSAENNIKMLSISDTPFIMVCPPSSPTFLNF 360 CC
CC 361 TQNVTFTSIFERCASTVVKLETILQKGLDKFLKGVLGMKDMPSLQFVKAQMLTMKS 420 CC
CC 361 TQNVTFTSIFERCASTVVKLETILQKGLDKFLKGVLGMKDMPSLQFVKAQMLTMKS 420 C
Db 361 TQNVTFTSIFERCASTVVKLETILQKGLDKFLKGVLGMKDMPSLQFVKAQMLTMKS 420 C
QY 421 KENCTNWSTIVLNLSNMNLTSVRCCLPPIKVLQDLSNSKIKSVPKVQVLEAQELNV 480 CC
DB 421 KENCTNWSTIVLNLSNMNLTSVRCCLPPIKVLQDLSNSKIKSVPKVQVLEAQELNV 480 C
QY 481 AFNSLTDLPGCGFSSLVLIHDNSVSHADSFFOSCQNSIKAGDNPFQTCERLF 540 CC
DB 481 AFNSLTDLPGCGFSSLVLIHDNSVSHADSFFOSCQNSIKAGDNPFQTCERLF 540 C
QY 541 VKNIDQSVSELEGWPDPSYKDYPESYRGSPKDFMSFMSNSCNITLIVGATMLVALV 600 CC
DB 541 VKNIDQSVSELEGWPDPSYKDYPESYRGSPKDFMSFMSNSCNITLIVGATMLVALV 600 C
QY 541 VKNIGWAREVEGWDSDSYRDYPESKGTLRDFMSPLSCDPTVLTGATMLVALV 600 CC
DB 541 VKNIGWAREVEGWDSDSYRDYPESKGTLRDFMSPLSCDPTVLTGATMLVALV 600 C
QY 601 TVTSLCYLDLFWYLRMWCOTOTRARRNPLELQRLNQPHAFISYSEHDSAWKSEL 660 CC
DB 601 TVTSLCYLDLFWYLRMWCOTOTRARRNPLELQRLNQPHAFISYSEHDSAWKSEL 660 C
QY 601 TGAFLCILYFDLFWYVRMLCOWTQTRHARHPLBLELQRNLQPHAFISYSEHDSAWKSEL 660 CC
DB 601 TGAFLCILYFDLFWYVRMLCOWTQTRHARHPLBLELQRNLQPHAFISYSEHDSAWKSEL 660 C
QY 661 UPYLEKDIQICLHERNFVPGKSIVENINCIEKSYKISIVLSPFQVSECHYELYFAH 720 CC
DB 661 UPYLEKDIQICLHERNFVPGKSIVENINCIEKSYKISIVLSPFQVSECHYELYFAH 720 C
QY 721 HNLFHEGSNNLILIPPIPONSIPIKYKULAMTOITYQWPKESKEKSKRSQFLWANTRA 780 CC
DB 721 HNLFHEGSNNLILIPPIPONSIPIKYKULAMTOITYQWPKESKEKSKRSQFLWANTRA 780 C
QY 781 FNMKLTUVTENDVKS 796 CC
DB 781 FNMKLTUVTENDVKS 796 C
QY 781 FMKMLALVNE-DDVKT 795 CC
DB 781 FMKMLALVNE-DDVKT 795 C

RESULT 12

ADU23195 ID ADU23195 standard; protein; 806 AA.
XX AC ADU23195;
XX DT 27-JAN-2005 (first entry)
XX DE Murine Toll-like receptor 6 (TLR6) protein - SEQ ID 87.
XX KW screening; Toll-like receptor agonist; TLR agonist; TLR6.
XX OS Mus sp.
XX PN WO2004094671-A2.
XX PD 04-NOV-2004.
XX PF 22-APR-2004; 2004WO-US012788.
XX PR 22-APR-2003; 2003US-0464586P.
PR 22-APR-2003; 2003US-0464588P.
PA (COLE-) COLEY PHARM GMBH.

QY 301 KITLKALTIETINQFLSQTAUYTFSENIMMLTISDTPFIMLCRPASTEKFLENF 360
DB 301 ETALKSMLIEHVKNQYFLSKPEALYSAENNIKMLSISDTPFIMVCPPSSPTFLNF 360 PA (COLE-) COLEY PHARM GROUP INC.
QY 361 TQNVTFTSIFERCASTVVKLETILQKGLDKFLKGVLGMKDMPSLQFVKAQMLTMKS 420 XX
DB 361 TQNVTFTSIFERCASTVVKLETILQKGLDKFLKGVLGMKDMPSLQFVKAQMLTMKS 420 PI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
XX DR WPI; 2004-795573/78.

QY 421 KENCTNWSTIVLNLSNMNLTSVRCCLPPIKVLQDLSNSKIKSVPKVQVLEAQELNV 480 XX
DB 421 KENCTNWSTIVLNLSNMNLTSVRCCLPPIKVLQDLSNSKIKSVPKVQVLEAQELNV 480 PS Disclosure; SEQ ID NO 87; 34pp; English.

QY 481 AFNSLTDLPGCGFSSLVLIHDNSVSHADSFFOSCQNSIKAGDNPFQTCERLF 540 XX
DB 481 AFNSLTDLPGCGFSSLVLIHDNSVSHADSFFOSCQNSIKAGDNPFQTCERLF 540 PT identifying agonists of Toll-like receptor (TLR) signaling activity,
PT useful therapeutically or prophylactically, comprises contacting an
PT RPM8226 cell that expresses a TIR with a test compound and measuring TIR
PT signalling activity.

QY 541 VKNIDQSVSELEGWPDPSYKDYPESYRGSPKDFMSFMSNSCNITLIVGATMLVALV 600 XX
DB 541 VKNIDQSVSELEGWPDPSYKDYPESYRGSPKDFMSFMSNSCNITLIVGATMLVALV 600 PT identifying agonists of Toll-like receptor (TLR) signaling activity,
PT useful therapeutically or prophylactically, comprises contacting an
PT RPM8226 cell that expresses a TIR with a test compound and measuring TIR
PT signalling activity.

QY 601 TVTSLCYLDLFWYLRMWCOTOTRARRNPLELQRLNQPHAFISYSEHDSAWKSEL 660 XX
DB 601 TVTSLCYLDLFWYLRMWCOTOTRARRNPLELQRLNQPHAFISYSEHDSAWKSEL 660 CC
QY 612 TGAFLCILYFDLFWYVRMLCOWTQTRHARHPLBLELQRNLQPHAFISYSEHDSAWKSEL 671 XX
DB 612 TGAFLCILYFDLFWYVRMLCOWTQTRHARHPLBLELQRNLQPHAFISYSEHDSAWKSEL 671 CC
QY 661 UPYLEKDIQICLHERNFVPGKSIVENINCIEKSYKISIVLSPFQVSECHYELYFAH 720 XX
DB 661 UPYLEKDIQICLHERNFVPGKSIVENINCIEKSYKISIVLSPFQVSECHYELYFAH 720 CC

QY	721	HNLFHEGSNNLILIPERIPONSPNPKHKLKALMTRYLQMPKEKSKRGLFWANIRAA	780	Db	672	LRLJEDDIRVCLHERNFVGKGSIVENINFLRKSKYAKIFVLSPHFQOSEWCHYELYFAH	731
QY	732	HNLFHEGSDNLILIPERIPONSPNPKHKLKALMTRYLQMPKEKSKRGLFWANIRAS	791	Db	673	HNLFHEGSDNLILIPERIPONSPNPKHKLKALMTRYLQMPKEKSKRGLFWANIRAS	791
QY	781	FNMKLTVTENDVKS	796	Db	674	FNMKLALVNE-DDVKT	806
QY	792	FNMKLALVNE-DDVKT	806	Db	675	FNMKLALVNE-DDVKT	806
RESULT 13				Db	676		
ID	AY88055	AY88055 standard; protein; 806 AA.		Db	677		
AC	XX			Db	678		
XX	AY88055;			Db	679		
DT	22-SEP-2000	(first entry)		Db	680		
DE	Murine Toll-like receptor TLR6 protein.			Db	681		
KW	Toll-like receptor; TLR6; murine; antiinfectious; treatment; infection; transcription factor; NF-kappaB; immune response.			Db	682		
OS	Mus sp.			Db	683		
PN	WO200024776-A1.			Db	684		
XX				Db	685		
XX				Db	686		
PP	26-OCT-1999; 99WO-JP0005917.			Db	687		
PR	26-OCT-1999; 98JP-00304110.			Db	688		
XX				Db	689		
PA	(NISC-) JAPAN SCI & TECHNOLOGY CORP.			Db	690		
PI	Akira S., Takeuchi O;			Db	691		
XX				Db	692		
DR	WPI; 2000-350697/30.			Db	693		
DR	N-PSDB; AAA39810.			Db	694		
PT	Toll-like receptor TLR6 molecule and encoded gene, participating in signal transduction of initial immune response, applicable e.g. in treating infections.			Db	695		
PT	Claim 1; Page 31-33; 35pp; Japanese.			Db	696		
XX				Db	697		
CC	This invention describes a novel toll-like receptor TLR6 which has antinfectious activity. The protein and its encoded gene have clinical use e.g. in treating infections. Toll family receptors are related to transcription factor NF-kappaB and regulate the expression of various genes participating in the immune response. This sequence represents the murine TLR6 protein which is described in the method of the invention			Db	698		
CC	Sequence 806 AA;			Db	699		
SQ	Query Match 75.6%; Score 3139.5; DB 3; Length 806; Best Local Similarity 73.7%; Pred. No. 1e-253; Matches 587; Conservative 98; Mismatches 110; Indels 1; Gaps 1;			Db	700		
QY	1	MTKDKETIVKSPHFWCMLITIVGTRLOFSDGMEFAYVKSKRQLIHVKDPLKTKYLDMS	60	Db	701		
Db	12	MSQDRKPDPIVGSFPHFVCAALIYGSMTPPSNELESMDYNSRNLLTHPKDLPLERTKAISLS	71	Db	702		
QY	61	ONYIAELQVSMSPLSFLSTVLSHARIQLQLSVFSYENQDLEYLQDISHNOKQSCHPI	120	Db	703		
Db	72	QNSISERKMPDSIFSLSERLVRLSRNRSLSPDPHFLPNQDLEYLQDISHNOKQSCHPI	131	Db	704		
QY	121	VSFRLHDLSFNPKALPICKFGNLQSQNLQKQDULPFLAHLHSYILLDRN	180	Db	705		
Db	132	ASLRHHLQSFNDPFDVLPVCKEFGNLQKQDULPFLAHLHSYILLDRN	191	Db	706		
QY	181	YYTKENETESTQILQNLAKTQLHLYFHFTSLFAIQVNISVNTLGCLQLNTKLNDDNCQVFIK	240	Db	707		
QY				Db	708		
RESULT 14				Db	709		
ID	ADU23194	ADU23194 standard; protein; 806 AA.		Db	710		
XX				Db	711		
AC	ADU23194;			Db	712		
XX				Db	713		
DT	27-JAN-2005	(first entry)		Db	714		
XX				Db	715		
DE	Murine Toll-like receptor 6 (TLR6) protein - SEQ ID 86.			Db	716		
XX				Db	717		
KW	screening; Toll-like receptor agonist; TLR agonist; TLR6.			Db	718		
XX				Db	719		
OS	Mus sp.			Db	720		
XX				Db	721		
PN	WO2004094671-A2.			Db	722		
XX				Db	723		
PD	04-NOV-2004.			Db	724		
XX				Db	725		
PF	22-APR-2004; 2004WO-US012788.			Db	726		
XX				Db	727		
PR	22-APR-2003; 2003US-0464586P.			Db	728		
PR	22-APR-2003; 2003US-0464588P.			Db	729		
XX				Db	730		
PA	(COLE-) COLEY PHARM GMBH.			Db	731		
PA	(COLE-) COLEY PHARM GROUP INC.			Db	732		
PI	Vollmer J., Jurk M., Liptord GB., Schetter C., Forsbach A., Krieg AM;			Db	733		
XX				Db	734		
WPI; 2004-795573/78.				Db	735		

XX
PT Identifying agonists of Toll-like receptor (TLR) signaling activity,
PT identifying therapeutically or prophylactically, comprises contacting an
PT RPM8226 cell that expresses a TLR with a test compound and measuring TLR
PT signaling activity.
XX
PS Disclosure; SEQ ID NO 85; 342pp; English.
XX
CC The invention comprises a screening method for identifying agonists of
CC Toll-like receptor (TLR) signalling activity. The method involves
CC contacting an RPM8226 cell (that expresses a TLR) with a test compound,
CC and measuring a test level of TLR signalling activity, where a test level
CC that is positive is indicative of a test compound that is a TLR agonist.
CC The method of the invention is useful for identifying agonists of TLR.
CC The present amino acid sequence represents a TLR protein.
XX
SQ Sequence 806 AA;

Query Match 75.6%; Score 3139.5; DB 8; Length 806;

Best Local Similarity 73.7%; Pred. No. 1e-253; Matches 587; Conservative 98; Mismatches 110; Indels 1; Gaps 1;

QY 1 MTKDKRPIVKSFHFCMLIMIVGTRIQFSDGNEFAVDKSKRGLIHPKDLPLKTKLDM 60
Db 12 MSQDRKPIVGSFFHFCMLALJVGSMWPFNSMLESMDYDSNNLTVPKDLPRTKALS 71
QY 61 ONYIAELQVSDMSFSELTVRLSHNRIOQLDLSVFKFNQDLEYDLSHNOQKTSCHPI 120
Db 72 QNSISBLRMPDISFSELVRVLRLSHNRIRSDFHFLFNQDLEYLDVSHNLQNISCCPM 131
QY 121 VSFRHDLISFDKFALPICKFGNISOLNFGLSAMKQCLDLPFLAHLISYILDLRN 180
Db 132 ASLRHDLISFDVLPVCKEFGNLTKLTFGLGSAKAFRDLLPVAHLHSCILDLVS 191
QY 181 YYIKENETESQIQLNAKTLHVPHPTSLFAIQVNISVNTLGCLQINTKUNDNCQFIK 240
Db 192 HHKGGETESQIOPNVTLHVPHFNSLSVQVNMSNALGHLOQNISIKNDENQRLMT 251
QY 241 FUSELJTRGSTLNFNTHNIETTWKCLVRFQFLWPKEVANINYNTIESIREEDFTY 300
Db 252 FUSELJTRGPTLNVHQIERTWKCSVYKLFQFPWMRPPVPEVANINYNTITERDREFTY 311
QY 301 KTTKLKALTIERITNDYFLESTALTYFSEANIMMUTISDPPIFHMLCPHAPRSTKFLNF 360
Db 312 ETALKSLMIEHVKNQVLFSEKALYSVFAEMNIMLSDIPFPIHVCPPSPSSFTLNP 371
QY 361 TQNVFDISFKECSTVKELETLQNGKLKFVGLIMTKDMSKPLSLEIDWSNSLSEGRH 420
Db 372 TQNVFDISVFGCSTUKRLQTLIOPNLGKPFKVALMTKMSLTDLYSINSLSHAY 431
QY 421 KENCTWVESTVNTLNSSNMLTDSVFRCLPPIRKVLDSHNKIKSVRQVVMKLAQELNV 480
Db 432 DRTCAWAESTLVNLNLSNMLTGSVFRCLPPIKVLDSHNKIMSPKDVTHLQAOELNV 491
QY 481 AFNSLTDLPGCGFSESSLVLTIDHNSVSHRADEFFOSCOKRSIKAGDNPFQCTBLREF 540
Db 492 ANSLTDLPGCGFSESSLVLTIDHNSVSHRADEFFOSCOKRSIKAGDNPFQCTBLREF 551
QY 541 VNIQDQSSELEGMDSYKDYPESYRGSLDKPIMSELSCLNITLIVGATMVLAV 600
Db 552 VENIGWAVAREVEGWDPSYRDYPESKGTALRDFHMSPLCDTBLTWTGATMVLAV 611
QY 601 TVTSCLCIYDIPWYLMRVCQTOTRRARNPYLELQRNQIOPHAFTSYSEHDSAWKSEL 660
Db 612 TGAFCLYFDLPWYVRLMCOMQTRRARNPYLELQRNQIOPHAFTSYSEHDSAWKSEL 671
QY 661 VPYLKEBDIQICLHERNVPKSIVENINIEKSKRISIFLSPNFWOSENCHYELYFAH 720
Db 672 LPNLKODDIRVCLHERNVPKSIVENINIEKSKRISIFLSPNFWOSENCHYELYFAH 731
QY 721 HNLFHGSNNLILREPIONSPNKYHKALMORTYQWPKKSKRSLFWANIRAA 780
Db 732 HNLFHGSNNLILREPIONSPSRYHKRALMAORTYQWPKKSKRSLFWANIRAS 791

QY 781 FNMKLTLVIENDVKS 796
Db 792 FIMKLALVNE-DDVKT 806

RESULT 15

ADU23196

ID ADU23196 standard; protein; 806 AA.

XX

AC ADU23196;

XX

DT 27-JAN-2005 (first entry)

XX

DE Murine Toll-like receptor 6 (TLR6) protein - SEQ ID 88.

XX

KW screening; Toll-like receptor agonist; TLR agonist; TLR6.

XX

OS Mus sp.

XX

PN WO2004094671-A2.

XX

PD 04-NOV-2004.

XX

BP 22-APR-2004; 2004WO-US012788.

XX

PR 22-APR-2003; 2003US-0464586P.

XX

BR 22-APR-2003; 2003US-0464588P.

XX

BA (COLE-) COLEY PHARM GMBH.

XX

DA (COLE-) COLEY PHARM GROUP INC.

XX

BI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;

XX

DR WPI; 2004-795573/7B.

XX

PT Identifying agonists of Toll-like receptor (TLR) signaling activity,

PT useful therapeutically or prophylactically, comprises contacting an

PT RPM8226 cell that expresses a TLR with a test compound and measuring TLR

PT signalling activity.

XX

PS Disclosure; SEQ ID NO 88; 342pp; English.

XX

The invention comprises a screening

CC method for identifying agonists of

CC Toll-like receptor (TLR) signalling activity. The method involves

CC contracting an RPM8226 cell (that expresses a TLR) with a test compound,

CC and measuring a test level of TLR signalling activity, where a test level

CC that is positive is indicative of a test compound that is a TLR agonist.

CC The method of the invention is useful for identifying agonists of TLR.

CC The present amino acid sequence represents a TLR protein.

XX

SQ Sequence 806 AA;

Query Match 75.6%; Score 3139.5; DB 8; Length 806;

Best Local Similarity 73.7%; Pred. No. 1e-253; Matches 587; Conservative 98; Mismatches 110; Indels 1; Gaps 1;

QY 1 MTKDKRPIVKSFHFCMLIMIVGTRIQFSDGNEFAVDKSKRGLIHPKDLPLKTKLDM 60
Db 12 MSQDRKPIVGSFFHFCMLALJVGSMWPFNSMLESMDYDSNNLTVPKDLPRTKALS 71
QY 61 ONYIAELQVSDMSFSELTVRLSHNRIOQLDLSVFKFNQDLEYDLSHNOQKTSCHPI 120
Db 72 QNSISBLRMPDISFSELVRVLRLSHNRIRSDFHFLFNQDLEYLDVSHNLQNISCCPM 131
QY 121 VSFRHDLISFDKFALPICKFGNISOLNFGLSAMKQCLDLPFLAHLISYILDLRN 180
Db 132 ASLRHDLISFDVLPVCKEFGNLTKLTFGLGSAKAFRDLLPVAHLHSCILDLVS 191
QY 181 YYIKENETESQIQLNAKTLHVPHPTSLFAIQVNISVNTLGCLQINTKUNDNCQFIK 240
Db 192 HHKGGETESQIOPNVTLHVPHFNSLSVQVNMSNALGHLOQNISIKNDENQRLMT 251

QY 241 FUSELTGSTLNLNFTLNIEITWKLCLVRVFRQTLWPKVEYNIYNTIESIREEDTYS 300
 Db 252 FUSELTGRPTLNVLQHETTMKCSYKLRFQFWPREVYNUJTERDREBFTYS 311
 QY 301 KTYKALTIETHTNQVFLPSOTALYTFSSEMMIMLTSIDTPTHMLCPHAPSTPKLNF 360
 Db 312 ETALKSLMIEHNQVLFPSKEALYSAFAEMIKMLSISDPFPIHMVCPPSPSSFFPLNF 371
 QY 361 TONVFTDSIEEKSTUJKLETILQOKGLPKVGMTKOMPSLETDVSNLSISGRH 420
 Db 372 TONVFTDSVFQGCTSKRLQTTLQRNGLKNPFKVALMTKMSLETIDVSLNSINSHAY 431
 QY 421 KENCTWVESIVVNLSSNMIDSVFRCLPPIKVLJHSNKSVPKQVKUBALQBLNV 480
 Db 432 DRTCAWESIULVNLSNMIGSVFRCLPPIKVLJHNRMSPDVTHIQALQBLNV 491
 QY 481 AFNSLTDLPGCSFSSLVSLVLLDHNNSYHPSADPFSCOKRSIKAGDNPOCTCEREP 540
 Db 492 ASNLSLTDLPGCAFSSLSVLDHNSYHPSDFPQSCONRSLTAGNNPFOCTCELDF 551
 QY 541 VENIDQSSVEUGWPSYKCYPESTRGSPKDFMSESCNTILITGATMVLAV 600
 Db 552 VENIGNWAREVEGWPSYRCDPPESSKGTLRDFHMSPLSCDTVLITVTGATMVLAV 611
 QY 601 TVTSCLCYLDLWYLRAWCQWTQRRARNTPLBLORNQPHAFISSESDSAWKSEL 660
 Db 612 TGAFLCYFDLWYVRLMCQWTRHARHTPLEBLORNQHAFISSESDSAWKEL 671
 QY 661 VPYLEKEDIQICLHERNVPKGSIVENINCIEKSYKSIYVSPNFEVOSENCHYELYFAH 720
 Db 672 LENLEKODDIRVCLHERNVPGKSIVENINFEXSYKAIFVSPHFIQSEWCHYELYFAH 731
 QY 721 HNLPHGGSNNLILILBIPONSIPNKYHKLMORTYQWPKESKRMFLWANTRAA 780
 Db 732 HNLPHGGSNDLILILBIPOLONIPSRYHKLPMALMORTYQWPKTEKGKRGULFWANTRAS 791
 QY 781 FMMKLTIVTENDVKS 796
 Db 792 FIMKLALVNE-DDVKT 806

Search completed: June 2, 2006, 22:54:52
 Job time : 114 secs

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2006, 23:11:41 ; Search time 1680 Seconds
(without alignments)

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: - Geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	
1	2753	100.0	2753	12 ADP56659	RESULT 1 ADP56659 ID ADP56659 standard; DNA; 2753 BP. AC ADP56659; XX
2	2753	100.0	2753	12 ADP48600	DT 09-SEP-2004 (first entry) XX
3	2753	100.0	2753	13 ADU23187	DE Human Toll-like receptor TLR6 DNA - SEQ ID 11. XX
4	2753	100.0	2753	14 ADX06215	KW expression system; Toll-like receptor; TLR6; immune response modifier; IRM; cancer; gene therapy; human; ds; gene. XX
5	2748.8	99.8	2760	6 ADU26300	KW OS Homo sapiens. XX
6	2748.8	99.8	2760	13 ADU23186	FH Key Location/Qualifiers FT CDS 67. 2457 FT /*tag= a FT /product= "Human Toll-like receptor TLR6 protein - SEQ ID 12" FT XX
7	2747.2	99.8	2760	3 AAX39809	PN WO2004053057-A2. XX
8	2727.8	99.1	2940	5 AAS44521	PD 24-JUN-2004. XX
9	2391	86.9	2391	14 ADV42616	PF 31-OCT-2003; 2003WO-US034563. XX
10	1533.6	55.7	2604	3 AAX39810	PR 11-DEC-2002; 2002US-0432651P. XX
11	1533.6	55.7	2604	13 ADU23191	DR (MINN) 3M INNOVATIVE PROPERTIES CO. XX
12	1533.5	55.7	2604	13 ADU23192	PA Aaa39809 Human Tol Ras44521 Human cDNA Adv42616 Human pSY Aaa39810 Murine To Adu23191 Murine To Adu23192 Murine To Adu23193 Murine To Adc78820 Human PRO Ade25536 Human TLR Adv42611 Human pSY Aav80663 Human DNA Aed26280 Human DNA XX
13	1531.2	55.6	2421	13 ADU23193	PT New expression system comprising a first nucleic acid sequence that encodes a toll-like receptor (TLR), useful for preparing a composition comprising TLR agonist for treating e.g., cancer. XX
14	1445	55.5	2381	10 ADC78820	PS Claim 3; SEQ ID NO 11; 69bp; English.
15	1444.2	52.5	2358	10 ADE25536	
16	1444.2	52.5	2361	14 ADV42611	
17	1444.2	52.5	2367	2 AAV80663	
18	1444.2	52.5	2367	6 AED26280	

XX
 CC The invention relates to a novel expression system comprising a first nucleic acid sequence that encodes a Toll-like receptor (TIR) operably linked to a first expression control sequence and a second nucleic acid sequence that encodes a reporter. TIRs are immune response modifiers (IRMs). The expression system of the invention may be useful for preparing a composition comprising the TIR agonist for treating cancer, possibly via gene therapy. The current sequence is that of the human Toll-like receptor TLR6 DNA (SEQ ID 11) of the invention.

CC
 CC
 CC
 CC Sequence 2753 BP; 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Matches 2753; Conservative 0;

Qy 1 AGAATTGGACTCATATCAAGATGCTCTGAAGAGAACACCCCTTAGGATAGCCACTGC 60
 Db 1 AGAATTGGACTCATATCAAGATGCTCTGAAGAGAACACCCCTTAGGATAGCCACTGC 60
 Qy 61 AACATCATGACAAAGACAAGAACCTATTGTTAAAGCTTCATTGTTGCTTATG 120
 Db 61 AACATCATGACAAAGACAAGAACCTATTGTTAAAGCTTCATTGTTGCTTATG 120
 Qy 121 ATCATAATAGTTGACCGAGAACATCCGGTCCGGAGGAATGAATTGCGTAGAACAG 180
 Db 121 ATCATAATAGTTGACCGAGAACATCCGGTCCGGAGGAATGAATTGCGTAGAACAG 180
 Qy 181 TCAAAGAGGCTTATCAGTCCAAAGAACCTACCGCTAACGCTAAACCAAGTCTAGAT 240
 Db 181 TCAAAGAGGCTTATCAGTCCAAAGAACCTACCGCTAACGCTAAACCAAGTCTAGAT 240
 Qy 241 ATGTCAGAACTACATGCTCAGCTCAGGTCTCTGACATAGCTTCTACAGATG 300
 Db 241 ATGTCAGAACTACATGCTCAGGTCTCTGACATAGCTTCTACAGATG 300
 Qy 301 ACCAGTTGACACTTCCATACAGATCCAGCTTCTGAAATGTTAAGTGTTCAGTTC 360
 Db 301 ACCAGTTGACACTTCCATACAGATCCAGCTTCTGAAATGTTAAGTGTTCAGTTC 360
 Qy 361 AACCAGATTAGAATTGGATTATCTATACTAGTGCAGAAAGATTCCTGCCAT 420
 Db 361 AACCAGATTAGAATTGGATTATCTATACTAGTGCAGAAAGATTCCTGCCAT 420
 Qy 421 CCTATGTTGAGTTTCAAGGATTAGATCTCATTCTATGATTCAAGGCTGCCATC 480
 Db 421 CCTATGTTGAGTTTCAAGGATTAGATCTCATTCTATGATTCAAGGCTGCCATC 480
 Qy 481 TGTAAAGGAAATTGGCAACTTACACACTGAAATTCTGGATTGAGTGCTATGAGCTG 540
 Db 481 TGTAAAGGAAATTGGCAACTTACACACTGAAATTCTGGATTGAGTGCTATGAGCTG 540
 Qy 541 CAAAATTAGATTGCTGCCATGCTCACTGCATCTAACTTATCTCTGGATTAA 600
 Db 541 CAAAATTAGATTGCTGCCATGCTCACTGCATCTAACTTATCTCTGGATTAA 600
 Qy 601 AGAAATTATAAAGAATGAGACAGAACGTTTACAAATTCTGATGCAAAACC 660
 Db 601 AGAAATTATAAAGAATGAGACAGAACGTTTACAAATTCTGATGCAAAACC 660
 Qy 661 CTTTACACTGTTTCAACCCAACTAGTTTACCTGACATTCAGTTAAT 720
 Db 661 CTTTACACTGTTTCAACCCAACTAGTTTACCTGACATTCAGTTAAT 720
 Qy 721 ACTTTAGGGTCTTCAACTACTAATTAATTGATGAGACTGCAAGTTTC 780
 Db 721 ACTTTAGGGTCTTCAACTACTAATTAATTGATGAGACTGCAAGTTTC 780
 Qy 781 ATTAATTTTATCAGACTCCAGAGTTCACCTTACCTGATGAGACATTCAGTTAAT 840
 Db 781 ATTAATTTTATCAGACTCCAGAGTTCACCTTACCTGATGAGACATTCACCCAC 840
 Qy 841 ATGAAACGACTTGGAAATGCCCTGGTCAGAGCTTCAATTCTGGCCAAACCTGTG 900

Db 841 ATAGAAACGACTTGGAAATGCCCTGGTCAGACTTGGCCAAACCTGTG 900
 Qy 901 GAATATTCATATTCAATTACATATTGAAAGCATTCGGAGAGATTACT 960
 Db 901 GAATATTCATATTCAATTACATATTGAAAGCATTCGGAGAGATTACT 960
 Qy 961 TATTCTAAAGACATTGAAAGCATTCAGACATTCAGGATTCGGAGAGATTACT 1020
 Db 961 TATTCTAAAGACATTGAAAGCATTCAGACATTCAGGATTCGGAGAGATTACT 1020
 Qy 1021 TTTCAGAGAGCTTGTACACCGTTCTGAGATGAGACATATGATGTTAACATT 1080
 Db 1021 TTTCAGAGAGCTTGTACACCGTTCTGAGATGAGACATATGATGTTAACATT 1080
 Qy 1081 TCGAGATACCTTTATACATGCTGTCCTCATGACCAAGCACATCAAGTITTG 1140
 Db 1081 TCGAGATACCTTTATACATGCTGTCCTCATGACCAAGCACATCAAGTITTG 1140
 Qy 1141 AACTTTACCCGAACGTTTCACAGATGATTGTTGAAATGTCACGGTAGTTAA 1200
 Db 1141 AACTTTACCCGAACGTTTCACAGATGATTGTTGAAATGTCACGGTAGTTAA 1200
 Qy 1201 TTGGAGACACTATCTACAAAAAATGGTTAAAGACCTTCAAGTAGTCTCATG 1260
 Db 1201 TTGGAGACACTATCTACAAAAAATGGTTAAAGACCTTCAAGTAGTCTCATG 1260
 Qy 1261 ACCAGAGATACTGCTTCTGGAAATACTGATGTTAGCTGTTGAAATCTGGT 1320
 Db 1261 ACCAGAGATACTGCTTCTGGAAATACTGATGTTAGCTGTTGAAATCTGGT 1320
 Qy 1321 AGACATAAGAAACTGACTGCGTTGAGAGTATAGTGGTTAAATRGTCTCAAT 1380
 Db 1321 AGACATAAGAAACTGACTGCGTTGAGAGTATAGTGGTTAAATRGTCTCAAT 1380
 Qy 1380 1381 ATGCTACTGACTCTTTCAGATGTTACCTCCAGGTCAAGGACTCTGAC 1440
 Db 1381 ATGCTACTGACTCTTTCAGATGTTACCTCCAGGTCAAGGACTCTGAC 1440
 Qy 1441 AGCAATAATAAGAGGCTCTAAAGCTGTTAAACTCTGGAAAGCTTGTCAAC 1500
 Db 1441 AGCAATAATAAGAGGCTCTAAAGCTGTTAAACTCTGGAAAGCTTGTCAAC 1500
 Qy 1500 1441 AGCAATAATAAGAGGCTCTAAAGCTGTTAAACTCTGGAAAGCTTGTCAAC 1500
 Db 1500 1501 AATGTTCTTCATTTTAACTGACTGACTCTCTGGATGTTGCGCAGTTAGCAGCTTCT 1560
 Qy 1560 1501 AATGTTCTTCATTTTAACTGACTGACTCTCTGGATGTTGCGCAGTTAGCAGCTTCT 1560
 Db 1560 1561 GATTCGATCATGATCACAACTTCACTGTTCCACCATGGCTGATTCTTCAGGGCTGC 1620
 Qy 1620 1561 GATTCGATCATGATCACAACTTCACTGTTCCACCATGGCTGATTCTTCAGGGCTGC 1620
 Db 1620 1621 CAGAAGTGGGTCAATAAGCAGGGGACATCCATCCTGGATTTCTTCAGAGCTG 1680
 Qy 1680 1621 CAGAAGTGGGTCAATAAGCAGGGGACATCCATCCTGGATTTCTTCAGAGCTG 1680
 Db 1680 1621 CAGAAGTGGGTCAATAAGCAGGGGACATCCATCCTGGATTTCTTCAGAGCTG 1680
 Qy 1680 1681 GAATTTGCTCAAATAATAGACCAACTTCACTGTTGAGGTGTTAGAGGGCTGGCTGATCT 1740
 Db 1681 GAATTTGCTCAAATAATAGACCAACTTCACTGTTGAGGTGTTAGAGGGCTGGCTGATCT 1740
 Qy 1740 1741 TTAAGTGTGACTTCCAGGAAGTTAGAGGAAGCCCTAAGGACTTCACTGCT 1800
 Db 1741 TTAAGTGTGACTTCCAGGAAGTTAGAGGAAGCCCTAAGGACTTCACTGCT 1800
 Qy 1800 1801 GAATTCTGTCACATTAACCTGCTGATGTCACCATCGTGCACCATGCTGGTGTG 1860
 Db 1860 1801 GAATTCTGTCACATTAACCTGCTGATGTCACCATCGTGCACCATGCTGGTGTG 1860
 Qy 1860 1861 GCTGTCAGTGACTCCCTGCTGATGTCACCATCGTGCACCATGCTGGTGTG 1920
 Db 1920 1861 GCTGTCAGTGACTCCCTGCTGATGTCACCATCGTGCACCATGCTGGTGTG 1920
 Qy 1920 1921 TCCGAGGACAGCTGGCGAGGGGGAGACATACCTGAGAGACTCAAAGA 1980

Db 1921 TCCAGCTGGACCCAGACTCGGGCAGGCCAGAACATACCTTAGAGACTCCAAAGA 1980
 Qy 1981 AACCTCCAGTTCATGCTTTATTCAATAGTGAATGATTCCTGCTGGTGAAAGT 2040
 Db 1981 AACCTCCAGTTCATGCTTTATTCAATAGTGAATGATTCCTGCTGGTGAAAGT 2040

Qy 2041 GATTTGGTACCTACCTAGAAAAGAGATACAGATTCTTCATGAGAAGACTT 2100
 Db 2041 GATTTGGTACCTACCTAGAAAAGAGATACAGATTCTTCATGAGAAGACTT 2100

Qy 2101 GTOCTCTGGCAAGAGCATGTG3AAAATATCAACTCACTGCAATGAGAAGTACAAGTCC 2160
 Db 2101 GTOCTCTGGCAAGAGCATGTG3AAAATATCAACTCACTGCAATGAGAAGTACAAGTCC 2160

Qy 2161 ATCTTGTGTTGCTCCAACTTGTGAGGTGAGTGTGTTCACTGAGATTA 2200
 Db 2161 ATCTTGTGTTGCTCCAACTTGTGAGGTGAGTGTGTTCACTGAGATTA 2200

Qy 2221 GCCCCATCACAACTCTTCATCAGAGCTAACTTAATCTCATCTCTGTGGACC 2280
 Db 2221 GCCCCATCACAACTCTTCATCAGAGCTAACTTAATCTCATCTCTGTGGACC 2280

Qy 2281 ATTCCACAGAACAGCATTCCTCAACAGACTAACTTAATCTCATCTGTGGAGGG 2340
 Db 2281 ATTCCACAGAACAGCATTCCTCAACAGACTAACTTAATCTCATCTGTGGAGGG 2340

Qy 2341 ACTTATTTGCACTGGGCCAACAGAAAGAACGAAACGTTGGCCTTTGGCTACATPAGA 2400
 Db 2341 ACTTATTTGCACTGGGCCAACAGAAAGAACGAAACGTTGGCCTTTGGCTACATPAGA 2400

Qy 2401 CGCGCTTTAATGAAATACACTGCTACTGAAACATGAACTGAACTCTAA 2460
 Db 2401 CGCGCTTTAATGAAATACACTGCTACTGAAACATGAACTGAACTCTAA 2460

Qy 2461 ATTAGGAATTCACCTAAAGAACATTATTACTTGATGATGATGAAATGAGT 2520
 Db 2461 ATTAGGAATTCACCTAAAGAACATTATTACTTGATGATGATGAAATGAGT 2520

Qy 2521 CGTAACTGAACTCTGGGACTGAGCTCTGGGACTCTGGGACTCTGGGACTCTGGG 2580
 Db 2521 CGTAACTGAACTCTGGGACTCTGGGACTCTGGGACTCTGGGACTCTGGGACTCTGGG 2580

Qy 2581 AACATAGTTCATCTGGGACTGAGCTGGGCTGGGTAGGTAGCTGGCTGGTAGAGAC 2640
 Db 2581 AACATAGTTCATCTGGGACTGAGCTGGGCTGGGTAGGTAGCTGGCTGGTAGAGAC 2640

Qy 2641 AGCCCAGTCTCTCTGGTTAACATCATTTGTTCAAATGAAACAGCTCTTGAGTAA 2700
 Db 2641 AGCCCAGTCTCTCTGGTTAACATCATTTGTTCAAATGAAACAGCTCTTGAGTAA 2700

Qy 2701 ATGCTCAGTTTCAGCTCCCTCACTCTCTTCCAAATGGATCTGTG 2753
 Db 2701 ATGCTCAGTTTCAGCTCCCTCACTCTCTTCCAAATGGATCTGTG 2753

RESULT 2
 ADP48600 standard; cDNA; 2753 BP.
 AC ADP48600;
 XX DT 09-SEP-2004 (first entry)
 DE Human Toll-like receptor 6 encoding cDNA SEQ ID NO:11.
 KW Toll-like receptor; TLR; human; detection; identification; TLR agonist;
 TLR antagonist; Toll like receptor 6; true; chromosome 4; gene; ss.
 OS Homo Sapiens.

Key Location/Qualifiers

FT CDS

/*tag= a

/product= "Toll-like receptor 6"
 FT XX
 PN WO2004053452-A2.
 XX PD 24-JUN-2004.
 XX PR 11-DEC-2002; 2002US-0432550P.
 XX PA (MINN) 3M INNOVATIVE PROPERTIES CO.
 PI Gupta SK, Ghosh TK, Fink JR;
 XX DR WPI: 2004-468955/44.
 DR P-PSDB; ADP48601.
 GENBANK; NM_006068.

PT Detecting activation of Toll-like receptors (TLR) for identifying a TLR
 agonist or antagonist, comprises providing a cell culture comprising
 PT cells transfected with a sequence encoding a reporter.

XX
 CC
 CC The present invention describes a method for detecting activation of a
 CC Toll-like receptor (TLR) in a cell. The method comprises: (a) providing a
 CC cell culture comprising cells transfected with a nucleic acid sequence
 CC that encodes a reporter that (i) generates a detectable signal when the
 CC reporter is expressed and the cell is exposed to conditions for
 CC generating the detectable signal, and (ii) is operably linked to an
 CC expression control sequence that is induced by activation of a TLR and
 CC comprises a cytokine promoter, a chemokine promoter, a co-stimulatory
 CC marker promoter, or a defensin promoter; (b) exposing the cell culture to
 CC a compound that activates a TLR; (c) providing conditions for generating
 CC the detectable signal; and (d) detecting the detectable signal. Also
 CC described: (1) a method of identifying a TLR agonist or antagonist;
 CC (2) a pharmaceutical composition comprising a TLR agonist or antagonist;
 CC (3) a pharmaceutical salt. The methods
 CC are useful for detecting activation of a TLR in a cell and for
 CC identifying TLR agonist or antagonist. The present sequence encodes a
 CC human TLR6 which is used in the exemplification of the present invention.
 CC The human TLR6 gene is located on chromosome 4, more specifically to
 CC 4p14.

Sequence 2753 BF; 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other;
 Query Match 100 0%; Score 2753; DB 12; Length 2753;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATTTGGACTCATATCAAGATGCTCTGGAGAGAACACCTTGTGGATAGCCACTGC 60
 Db 1 AGATTTGGACTCATATCAAGATGCTCTGGAGAGAACACCTTGTGGATAGCCACTGC 60

Qy 61 AACATCATGACAAAGAACCTATGTTAAAGCTCCATTGTTGCGCTTATG 120
 Db 61 AACATCATGACAAAGAACCTATGTTAAAGCTCCATTGTTGCGCTTATG 120

Qy 121 ATCATATAGTTGGACGAGAACATCCAGTCTCCGAGGAATGATTGAGTACAG 180
 Db 121 ATCATATAGTTGGACGAGAACATCCAGTCTCCGAGGAATGATTGAGTACAG 180

Qy 181 TCAAAAGAGCTTATCTGTCAGAACAGCTTACCGCTGAAACAAAGCTTGTAG 240
 Db 181 TCAAAAGAGCTTATCTGTCAGAACAGCTTACCGCTGAAACAAAGCTTGTAG 240

Qy 241 ATGCTCAGACTACATCGCTGAGCTTGTGAGCTTCTATCAGAGTG 300
 Db 241 ATGCTCAGACTACATCGCTGAGCTTGTGAGCTTCTATCAGAGTG 300

Qy 301 ACAGTTGAGACTTCCCTAACAGATCCAGTACTCTGTTAGTGTTCAGTRC 360

Db	301	ACAGTTTGAGACTTCCCATACAGAACATCCAGCTACTGTAAAGGTTCAGTC	360	Qy	1441	ACGATAATAAAGAGCGGTCTAACAGTCGAACCTGGAACTTGCAGAACTC	1500
Qy	361	ACCAAGATTAGAATTGATTGATTATCTCTAACTCAGTCAGTCAGTCAGTC	420	Db	1441	ACGATAATAAAGAGCGGTCTAACAGTCGAACCTGGAACTTGCAGAACTC	1500
Db	361	ACCAAGATTAGAATTGATTGATTATCTCTAACTCAGTCAGTCAGTCAGTC	420	Qy	421	CCTATGAGTTAGGCAATTAGTAGCTCTCATCAATGAGTCAGTCAGTCAGTC	480
Qy	421	CCTATGAGTTAGGCAATTAGTAGCTCTCATCAATGAGTCAGTCAGTCAGTC	480	Db	421	CCTATGAGTTAGGCAATTAGTAGCTCTCATCAATGAGTCAGTCAGTCAGTC	480
Qy	481	TGTAAGAATTGGCAACTTACACACTGAACTTACACTGAACTTACACTGAA	540	Db	481	TGTAAGAATTGGCAACTTACACACTGAACTTACACTGAACTTACACTGAA	540
Db	481	TGTAAGAATTGGCAACTTACACACTGAACTTACACTGAACTTACACTGAA	540	Qy	541	CAAATTAGTTGCTGCCATGCTACTGCTACTGCTACTGCTACTGCTACTG	600
Qy	541	CAAATTAGTTGCTGCCATGCTACTGCTACTGCTACTGCTACTGCTACTG	600	Db	541	CAAATTAGTTGCTGCCATGCTACTGCTACTGCTACTGCTACTGCTACTG	600
Qy	601	AGAAATTATTAATAAGAAATGAGACAGAACATCTGAATGCAAACACC	660	Db	601	AGAAATTATTAATAAGAAATGAGACAGAACATCTGAATGCAAACACC	660
Db	601	AGAAATTATTAATAAGAAATGAGACAGAACATCTGAATGCAAACACC	660	Qy	661	CTTCACTGTTGCCACTAGTTGCTATCCAGTGAACATTCAGTAACTCAGTAA	720
Qy	661	CTTCACTGTTGCCACTAGTTGCTATCCAGTGAACATTCAGTAACTCAGTAA	720	Db	661	CTTCACTGTTGCCACTAGTTGCTATCCAGTGAACATTCAGTAACTCAGTAA	720
Db	720	CTTCACTGTTGCCACTAGTTGCTATCCAGTGAACATTCAGTAACTCAGTAA	720	Qy	721	ACTTGGGCTTACAACCTAACTATTAATTGATGAGCAACTGCAAGTTTC	780
Qy	721	ACTTGGGCTTACAACCTAACTATTAATTGATGAGCAACTGCAAGTTTC	780	Db	721	ACTTGGGCTTACAACCTAACTATTAATTGATGAGCAACTGCAAGTTTC	780
Db	780	ACTTGGGCTTACAACCTAACTATTAATTGATGAGCAACTGCAAGTTTC	780	Qy	781	ATTAATTTATCAGAACCTAACACAGGTTAACCTACTGAAATTACCTAAC	840
Qy	781	ATTAATTTATCAGAACCTAACACAGGTTAACCTACTGAAATTACCTAAC	840	Db	781	ATTAATTTATCAGAACCTAACACAGGTTAACCTACTGAAATTACCTAAC	840
Qy	840	ATAGAACGACTGGAATGCTGCGAGAACCTAACCTGAACTTACCTAAC	900	Db	840	ATAGAACGACTGGAATGCTGCGAGAACCTAACCTGAACTTACCTAAC	900
Db	900	ATAGAACGACTGGAATGCTGCGAGAACCTAACCTGAACTTACCTAAC	900	Qy	901	GAATATCTCAATTACAACTAACATAATGAAAGCATCTGAGAGAATTACT	960
Qy	901	GAATATCTCAATTACAACTAACATAATGAAAGCATCTGAGAGAATTACT	960	Db	901	GAATATCTCAATTACAACTAACATAATGAAAGCATCTGAGAGAATTACT	960
Db	960	GAATATCTCAATTACAACTAACATAATGAAAGCATCTGAGAGAATTACT	960	Qy	961	TATTCAGAGAACATGAAAGCATGAACTAACATACGACCAAGTTCTG	1020
Qy	961	TATTCAGAGAACATGAAAGCATGAACTAACATACGACCAAGTTCTG	1020	Db	961	TATTCAGAGAACATGAAAGCATGAACTAACATACGACCAAGTTCTG	1020
Qy	1020	TATTCAGAGAACATGAAAGCATGAACTAACATACGACCAAGTTCTG	1020	Db	1020	TATTCAGAGAACATGAAAGCATGAACTAACATACGACCAAGTTCTG	1020
Db	1020	TATTCAGAGAACATGAAAGCATGAACTAACATACGACCAAGTTCTG	1020	Qy	1021	TTTCACTGAGAGCTTGTACACGGTTCTGACATGACATTGACATTGAC	1080
Qy	1021	TTTCACTGAGAGCTTGTACACGGTTCTGACATGACATTGACATTGAC	1080	Db	1021	TTTCACTGAGAGCTTGTACACGGTTCTGACATGACATTGACATTGAC	1080
Db	1080	TTTCACTGAGAGCTTGTACACGGTTCTGACATGACATTGACATTGAC	1080	Qy	1081	TCAGATACACCTTATACACATGCTGCTCATCCACCAACATCAAGTTTG	1140
Qy	1081	TCAGATACACCTTATACACATGCTGCTCATCCACCAACATCAAGTTTG	1140	Db	1081	TCAGATACACCTTATACACATGCTGCTCATCCACCAACATCAAGTTTG	1140
Db	1140	TCAGATACACCTTATACACATGCTGCTCATCCACCAACATCAAGTTTG	1140	Qy	1141	ACTTTACCCGAGACGGTTACAGATGAAATTGAAAGATGCTACGTTAA	1200
Qy	1141	ACTTTACCCGAGACGGTTACAGATGAAATTGAAAGATGCTACGTTAA	1200	Db	1141	ACTTTACCCGAGACGGTTACAGATGAAATTGAAAGATGCTACGTTAA	1200
Db	1200	ACTTTACCCGAGACGGTTACAGATGAAATTGAAAGATGCTACGTTAA	1200	Qy	1201	TGGAGACACTATCTACAAAAAATGGATAAAGACCTTCAAGTAGGTCTCATG	1260
Qy	1201	TGGAGACACTATCTACAAAAAATGGATAAAGACCTTCAAGTAGGTCTCATG	1260	Db	1201	TGGAGACACTATCTACAAAAAATGGATAAAGACCTTCAAGTAGGTCTCATG	1260
Db	1260	TGGAGACACTATCTACAAAAAATGGATAAAGACCTTCAAGTAGGTCTCATG	1260	Qy	1261	ACGAAGATATGCCCTTGTGAACTGCTGCTGCTGCTGCTGCTGCTGCTG	1320
Qy	1261	ACGAAGATATGCCCTTGTGAACTGCTGCTGCTGCTGCTGCTGCTGCTG	1320	Db	1261	ACGAAGATATGCCCTTGTGAACTGCTGCTGCTGCTGCTGCTGCTGCTG	1320
Db	1320	ACGAAGATATGCCCTTGTGAACTGCTGCTGCTGCTGCTGCTGCTGCTG	1320	Qy	1321	ACGATAAGAACACTGGCACTGGGTGAGGATAGTGGTTAACTGCTCAAT	1380
Qy	1321	ACGATAAGAACACTGGCACTGGGTGAGGATAGTGGTTAACTGCTCAAT	1380	Db	1321	ACGATAAGAACACTGGCACTGGGTGAGGATAGTGGTTAACTGCTCAAT	1380
Db	1380	ACGATAAGAACACTGGCACTGGGTGAGGATAGTGGTTAACTGCTCAAT	1380	Qy	1381	ATGCTACTGACTCTTGTAGATCTTACTCCAGGACAAAGTACTGATCTCAC	1440
Qy	1381	ATGCTACTGACTCTTGTAGATCTTACTCCAGGACAAAGTACTGATCTCAC	1440	Db	1381	ATGCTACTGACTCTTGTAGATCTTACTCCAGGACAAAGTACTGATCTCAC	1440

2521 CGTAACTGTTGAGGTGGCTTCATTCCTCATGCTTCAGGAAGACTTACAA 2580
 Db 61 AACATCATGACAGAACAGAACCTATGTTAAGCTTCATTITGTCCTATG 120
 Qy 121 ATCATAATAGTTGGACCAAGATCCAGTTCCGAGGAAATGAATTGCGTAGACAG 180
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 Db 181 TCAAAGAGGCTTATCGTTCAGTTCAAAGACCTACCGCTGAAACCAAGTCTAGAT 240
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 Qy 361 ACCAGGATTAGATAATTGGATTATCTCATACGTGCAAGAGATTCCTGCCAT 420
 Db 361 ACCAGGATTAGATAATTGGATTATCTCATACGTGCAAGAGATTCCTGCCAT 420
 DT 421 CCTATGTGAGTTAGGCATTAATGCTCATTCATCAATGTTCAAGGCTGCCCAC 480
 Qy 421 CCTATGTGAGTTAGGCATTAATGCTCATTCATCAATGTTCAAGGCTGCCCAC 480
 XX Human Toll-like receptor 6 (TLR6) cDNA sequence - SEQ ID 79.
 DE 481 TGTTAGGAATTGCAACTTACAACAGTCAATTCTGCTCAATGTTCAAGGCTGCCCAC 540
 KW screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.
 OS Homo sapiens.
 PN WO2004094671-A2.
 XX
 XX
 XX
 PR 22-APR-2004; 2004WO-US012788.
 PR 22-APR-2003; 2003US-0464586P.
 PR 22-APR-2003; 2003US-0464588B.
 PA (COLE-) COLEY PHARM GMBH
 PA (COLE-) COLEY PHARM GROUP INC.
 RI Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;
 XX DR WPI; 2004-795573/78.
 XX
 PT Identifying agonists of Toll-like receptor (TIR) signalling activity, comprises contacting an RPMI8266 cell that expresses a TIR with a test compound and measuring TIR signalling activity.
 PT Disclosure; SEQ ID NO 79; 342pp; English.
 CC The invention comprises a screening method for identifying agonists of Toll-like receptor (TIR) signalling activity. The method involves contacting an RPMI8266 cell (that expresses a TIR) with a test compound, and measuring a test level of TIR signalling activity, where a test level that is positive is indicative of a test compound that is a TIR agonist. The method of the invention is useful for identifying agonists of TIR. The present nucleic acid represents a TIR cDNA sequence.
 CC Sequence 2753 BP; 849 A; 559 C; 507 G; 838 T; 0 U; 0 other;
 SQ Query Match 100.0%; Score 2753; DB 13; Length 2753;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 AGATTGAGACTATCAGATGCTCTGAAAGAGAACCTTGTAGGATGCCCTGC 60
 1 AGATTGAGACTATCAGATGCTCTGAAAGAGAACCTTGTAGGATGCCCTGC 60
 Qy 61 AACATCTGACCAAGACAAGAACCTATGTTAAAGCTTCATTGTTGCTTATG 120
 Db 61 AACATCTGACCAAGACAAGAACCTATGTTAAAGCTTCATTGTTGCTTATG 120

Db	1141	AACTTTACCCSGAACCTTTACAGATAGTATTGAAAMATGTTCCAGGTAGTAA	1200	Oy	2281	ATCCACAGACACCATCCAAACAGTCAGAGTCAGGCCAGCG	2340
Qy	1201	TGGAGACACTATCTACAAAAAATGGATAAAAGACCTTTCAAGTGGCTCATG	1260	Db	2281	ATTCACAGACAGCATTCACACAGTACCAAGCTGAGGCCTCATGACCGCG	2340
Db	1201	TGGAGACACTATCTACAAAAAATGGATAAAAGACCTTTCAAGTGGCTCATG	1260	Oy	2341	ACTTATTGGAGTGGCCCAAGGAGAAAGCAACTGGGCTTTGGCTAACATTGA	2400
Qy	1261	ACGAAGGATAGCCCTTGGAAATACTGAGTGTAGCTGAGTAATTGGAACTTG	1320	Db	2341	ACTTATTGGAGTGGCCCAAGGAGAAAGCAACTGGGCTTTGGCTAACATTGA	2400
Db	1261	ACGAAGGATAGCCCTTGGAAATACTGAGTGTAGCTGAGTAATTGGAACTTG	1320	Oy	2401	GCCGCTTTATGAAATACAGTCACTGACTGAAACAATGATGTTGAATCTAA	2460
Qy	1321	AGACATAAGAAACTGCACTTGGGTGAGGTATAGTGGTAATTGCTCAAT	1380	Db	2401	GCCGCTTTATGAAATACAGTCACTGACTGAAACAATGATGTTGAATCTAA	2460
Db	1321	AGACATAAGAAACTGCACTTGGGTGAGGTATAGTGGTTAACATTGCTCAAT	1380	Oy	2461	AATTAGAAATCACTTAAAGAACCTTATTACTSGATGATGGTAGACTACAST	2520
Qy	1381	ATGCTACTGACTCTGTTAGATTTACTCCAGGATCAAGGACTTGTACITCAC	1440	Db	2461	AATTAGAAATCACTTAAAGAACCTTATTACTGGATGTTGAGTAGTACAGT	2520
Db	1381	ATGCTACTGACTCTGTTAGATTTACTCCAGGATCAAGGACTTGTACITCAC	1440	Oy	2521	CCTAAGTACTGCTGGAGTGGCTCCATATCTCAGCTCTCAGGAAAGACTAAC	2580
Qy	1441	AGCAATAAAAGAGGGCTCTAAACAAGCTGAAACTGGAACCTTCAGACTC	1500	Db	2521	CCTAAGTACTGCTGGAGTGGCTCCATATCTCAGCTCTCAGGAAAGACTAAC	2580
Db	1441	AGCAATAAAAGAGGGCTCTAAACAAGCTGAAACTGGAACCTTCAGACTC	1500	Oy	2581	AAACAGTGTACCTGGAAACTGAGCTAGCTGGGTGAGTTAGCTGCAGTTAACAA	2640
Qy	1501	AATGTCCTTCAATTCTTAACTGACCTTCTGGATGTCGAGCTTGGCCCTT	1560	Db	2581	AAACAGTGTACCTGGAAACTGAGCTAGCTGGGTGAGTTAGCTGCAGTTAACAA	2640
Db	1501	AATGTCCTTCAATTCTTAACTGACCTTCTGGATGTCGAGCTTGGCCCTT	1560	Oy	2641	AGCCAGTCCTCTGGTAACTGATGCTGAGCTTCAGAGACTTAA	2700
Qy	1561	GTATTGATCATGATCAACATTCAGTTCCACCCATGGTCTCAGAGCTGC	1620	Db	2641	AGCCAGTCCTCTGGTAACTGATGCTGAGCTTCAGAGACTTAA	2700
Db	1561	GTATTGATCATGATCAACATTCAGTTCCACCCATGGTCTCAGAGCTGC	1620	Oy	2701	ATGTCAGTTTCACTCCCTCCACTCTGCTTCCAAATGATTCTGTTG	2753
Qy	1621	CAGAAAGTGAAGCTAAAGCAGGAGCAATCCATTCAGTACCTGGAGCTA	1680	Db	2701	ATGTCAGTTTCACTCCCTCCACTCTGCTTCCAAATGATTCTGTTG	2753
Db	1621	CAGAAAGTGAAGCTAAAGCAGGAGCAATCCATTCAGTACCTGGAGCTA	1680	RESULT 4			
Qy	1681	GAATTGTCAAATAATAGACCAAGTACAGTGAAGTGTAGAGGCTGCTGATCT	1740	ID	ADX06215		
Db	1681	GAATTGTCAAATAATAGACCAAGTACAGTGAAGTGTAGAGGCTGCTGATCT	1740	ID	ADX06215	standard; DNA; 2753 BP.	
Qy	1741	TATAAGTGTGACTTACCGAGAAGTTAGAGGAGGCCACTAAAGGACTTCAATGCT	1800	XX	AC	ADX06215;	
Db	1741	TATAAGTGTGACTTACCGAGAAGTTAGAGGAGGCCACTAAAGGACTTCAATGCT	1800	XX	DT	21-APR-2005 (first entry)	
Qy	1801	GAATTATCCTGACACATAACTCTGCTACCTGTCACCATCG3GCCACCATCTGGTTG	1860	XX	DE	Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 780.	
Db	1801	GAATTATCCTGACACATAACTCTGCTACCTGTCACCATCG3GCCACCATCTGGTTG	1860	XX	FR	cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.	
Qy	1861	GTGTGACTGTGACTCCCTCGATCTACTGGATCTGCCTGGTATCTAGGGTGTG	1920	XX	OS	Homo sapiens.	
Db	1861	GTGTGACTGTGACTCCCTCGATCTACTGGATCTGCCTGGTATCTAGGGTGTG	1920	DN	W02005012875-A2.		
Qy	1921	TOCCAGTGGACCCAGACTGGGCCAGGAACTACCCCTAGAGAACCTCAAAGA	1980	XX	PR	29-JUL-2003; 2003US-0490890P.	
Db	1921	TOCCAGTGGACCCAGACTGGGCCAGGAACTACCCCTAGAGAACCTCAAAGA	1980	XX	PR	10-FEB-2005.	
Qy	1981	AACTTCCAGTTACCTGATCTGCTTATTCTATAGTGAATGATCTGCTGCTGATG	2040	XX	PR	29-JUL-2004; 2004WO-US024424.	
Db	1981	AACTTCCAGTTACCTGATCTGCTTATTCTATAGTGAATGATCTGCTGCTGATG	2040	XX	PA	(BRIM) BRISTOL-MYERS SQUIBB CO.	
Qy	2041	GAATTGGTACCTTACCTGAGAAAGGATATACAGATTGCTTCATGAGGAACTT	2100	XX	PI	Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;	
Db	2041	GAATTGGTACCTTACCTGAGAAAGGATATACAGATTGCTTCATGAGGAACTT	2100	XX	DR	WPI; 2005-163088/17.	
Qy	2101	GTCCCTGGCAAGAGCATGGGAAATATCACTGATGAGAGGAGTACAGTC	2160	XX	P-PSDB;	ADX06216.	
Db	2101	GTCCCTGGCAAGAGCATGGGAAATATCACTGATGAGAGGAGTACAGTC	2160	XX	PS	Biomarkers useful for predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclin-dependent kinase activity.	
Qy	2161	ATCTTGTGTTCTCCACATTGTGCAAGAGTGTGGCTCATGAGAGTACAGTC	2220	XX	CC	This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from	
Db	2221	GCCCATCACACTCTTCACTGAGGATCTAATCTCACTTGTGGACCC	2280	XX			
Qy	2221	GCCCATCACACTCTTCACTGAGGATCTAATCTCACTTGTGGACCC	2280				

CC 274 biomarkers given in the specification (nucleotide sequence SEQ ID NO:246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent, modulating cdk activity. The invention also describes a method for disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-5-[5-(1,1-Dimethylethyl)-2-oxazolyl(methyl)thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-1% sequence encodes a biomarker used in the method of the invention.

SQ

Sequence 2753 BP; 849 A; 559 C; 507 G; 838 T; 0 U; 0 Other;
 Query Match 100%; Score 2753; DB 14; Length 2753;
 Best Local Similarity 100%; Pred. No.; Mismatches 0; Indels 0; Gaps 0;
 Matches 2753; Conservative 0; QY
 1 AGAATTGGACTCATCAAGATGCTCTGAAGAGACACACCTTAGGATGCCACTGC 60
 Db 1 AGAATTGGACTCATCAAGATGCTCTGAAGAGACACACCTTAGGATGCCACTGC 60
 QY 61 AACATCATGACAAAGACAAAGACAAAGACACTTGTAAAGCTTCATTTGTTGCCPTATG 120
 Db 61 AACATCATGACAAAGACAAAGACACTTGTAAAGCTTCATTTGTTGCCPTATG 120
 QY 121 ATCATATAGCTGGACCAGATCCAGTCTCCGACCGAAATGAATTGCGTAGACAAG 180
 Db 121 ATCATATAGCTGGACCAGATCCAGTCTCCGACCGAAATGAATTGCGTAGACAAG 180
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 QY 241 ATGCTCTAGACTATCAGCTCTGAGCTTCAGAGCTTCTAG 300
 Db 241 ATGCTCTAGACTATCAGCTCTGAGCTTCAGAGCTTCTAG 300
 QY 301 ACAGTTGAGACTTCCATAACAGATCCAGACTTGTTAGTGTTCAGTC 360
 Db 301 ACAGTTGAGACTTCCATAACAGATCCAGACTTGTTAGTGTTCAGTC 360
 QY 361 ACCAGGATTAGAAATTGGATTATCTCTAACTAGTGCAGAACAGATCCGCCAT 420
 Db 361 ACCAGGATTAGAAATTGGATTATCTCTAACTAGTGCAGAACAGATCCGCCAT 420
 QY 421 CCTATGTTGAGTTCTGGCTTCAAGGCTCTGCCATC 480
 Db 421 CCTATGTTGAGTTCTGGCTTCAAGGCTCTGCCATC 480
 QY 481 TGTAAAGATTGGCAACTTACACACTGATTCTGGATTGAGTGTGCTATGGCT 540
 Db 481 TGTAAAGATTGGCAACTTACACACTGATTCTGGATTGAGTGTGCTATGGCT 540
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 Db 541 CAAAATTAGTTGGCTCATGCTCACITGCATCTAACTGTTCTGGATTA 600
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 Db 601 AGAAATTATTAAGAAATGAGACAGAACTCTGAAACCC 660
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 Db 721 ACTTAAAGGCTTACACTAATTAATGATGAGTGTGACACTCTCAAGTTTC 780

QY 781 ATTAATTTPATCAGACTCACCAGGTTCAACCTTACTGAATTACCTCAACAC 840
 Db 781 ATTAATTTPATCAGACTCACCAGGTTCAACCTTACTGAATTACCTCAACAC 840
 QY 841 ATAGAACACTTGGAAATGCTGGTCAAGTCTTCAATTTCGCCCACACTTG 900
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 Db 961 TATCTPAAAGACATGTTGAAAGCATGTTAGAACATACGRACCAAGTTCTG 1020
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 Db 1081 TCAGATACCTTATACAGATGCTGTTCTAGTCACTGACCAAGACATCAAGTTG 1140
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 QY 1381 ATGCTTACTGACTCTTTCAGATTTGAGGTTGAGGATGTTGGTTAAATGCT 1440
 Db 1381 ATGCTTACTGACTCTTTCAGATTTGAGGTTGAGGATGTTGGTTAAATGCT 1440
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 QY 2581 AACAACTGTTCTCATCGGGACTGAGCTGAGCTGGCTGGCTAGGAGAC 2640
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 QY 2641 AGCCCACTCTCTGGTTATCATATGTTCAATTGAAACAGCTCTTGTGAA 2700
 Db 2701 ATGCTCAAGTTTCAGTCCTCCACTCTGCTTCCAAATGGATCTGTG 2753
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RESULT 5

AAD26300 ID AAD26300 standard; cdna; 2760 bp.

XX Homo sapiens.

OS

XX

FH

KEY

CD5

68 . 2458

*tag= a

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 (transl except (pos=593 . 646 aa-heu-1le)
 note= "This translational exception occur while decoding
 for the alternative version of DTLR9 (AAU1612)"

FT

FT

FT

sig_peptide

69 . 160

/tag= b

mat_peptide

1st. . 2455

/*tag= C

/product= "Human mature DTLR9 and its alternative
 version"

FT

FT

FT

XX

PN WO200190151-A2.

XX

PD 29-NOV-2001.

XX

PP 23-MAY-2001; 2001WO-US016766.

XX

PR 25-MAY-2000; 2000US-0207558P.

XX

PA (SCHIE) SCHERING CORP.

XX

PJ Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;

XX

DR WPI; 2002-083085/11.

XX

P-PSDB; AAE16109, AAE16112.

XX

CC New DNAx Toll like receptor (DTLR) Proteins, useful for treating
 conditions exhibiting abnormal expression of the receptors of their
 ligands, particularly abnormalities manifested by immunological
 disorders.

XX

PS Claim 16; Page 72-75; 29pp; English.

XX

The invention relates to mammalian receptor proteins, e.g., primate,
 human DNAx Toll like receptor (DTLR) protein and their corresponding
 nucleic acids. The DTLR is useful for treating conditions exhibiting
 abnormal expression of the receptors of their ligands. Such abnormality
 is manifested by immunological disorders. In particular, the DTLR is
 useful for treating various disease or disorders associated with abnormal
 expression or abnormal triggering of response to a ligand. The DTLR is
 also useful as an immunogen for the production of antisera or antibodies
 specific, e.g. capable of distinguishing between other interleukin (IL)-1
 receptor family members, for the DTLR or its various fragments. The
 purified DTLR can be used to screen monoclonal antibodies or antigen-
 binding fragments. The antibodies are useful for screening expression
 libraries for particular expression products. These are useful for
 detecting or diagnosing various immunological conditions related to
 expression of DTLR or cells that express it. The present sequence is
 human DTLR9 cDNA

XX

Sequence 2760 BP; 850 A; 560 C; 511 G; 838 T; 0 U; 1 Other;
 SQ

Query Match 99 %; Score 2748.8; DB 6; Length 2760;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 3; Indels 0; Gaps 0;
 Matches 2750; Conservative 0;

QY 1 AGAATTGGACTCATCATGATGTCGAGAGAACACCTTGTAGATGCCACTGC 60
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QY 61 AACATATAGTGGACCAAGAACAAAGAACCTTGTAAAGCTCCATTGTTGCCTT 120
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QY 121 ATCATATAGTGGACCAAGAACAAAGAACCTTGTAAAGCTCCATTGTTGCCTT 180
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KW Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
 interleukin 1; IL-1; screening; immunomodulator; ss.

QY 181 TCAAAAGAGCTTATCAGTCAGTCAGGAAACTCGCTGAAACCAAAGCTTAGAT 240
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 Db 782 ATTAAATTATGAGCAACTACCAGAGGTCACCTACTGTTACCTCACCC 841
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 QY 901 GAAATCTCAATTACAATTACAATAATGAAAGCATCTGAGAGATTACT 960
 Db 902 GAATATCTCAATTACAATTACAATAATGAAAGCATCTGAGAGATTACT 961
 QY 961 TATTCTAAAGACATGAAAGCATGAACTAGACATATCACGACCAAGTTCTG 1020
 Db 962 TATTCTAAAGACATGAAAGCATGAACTAGACATATCACGACCAAGTTCTG 1021
 QY 1021 TTTCAGAGCAGCTTGTGAGACCGTTCTGAGCTGACATATGAGTTAACATT 1080
 Db 1022 TTTCAGAGCAGCTTGTGAGACCGTTCTGAGCTGACATATGAGTTAACATT 1081
 QY 1081 TCAGATACACCTTATACAGTCGCTGCTCATGCCAACATTCAAGTTG 1140
 Db 1082 TCAGATACACCTTATACAGTCGCTGCTCATGCCAACATTCAAGTTG 1141
 QY 1141 ACTTACCCAGAACGGTTACAGTAGTTTGTGAAAGATGTCACCTTAA 1200
 Db 1142 ACTTACCCAGAACGGTTACAGTAGTTTGTGAAAGATGTCACCTTAA 1200
 QY 1201 TTGGAGACACTTCTACAAAAATGGATAAGACCTTCAAGTAGGTCTCATG 1260
 Db 1202 TTGGAGACACTTCTACAAAAATGGATAAGACCTTCAAGTAGGTCTCATG 1261
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 Db 1262 ACCAAGGATACCTTCTGGAAACTCTGGATTTGGATCTGGATCTGGT 1321
 QY 1321 AGACATAAGAAACTCCTGAGCTTCTGAGCTTCTGAGCTTCTGAAAT 1380
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 Db 1922 TGCCAGTGGACCCAGACTCGGCGACGGCCAGGGACATACCTTAGAGAACTCCAA 1981
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 Db 1982 AACCTCAGTTCTACCTTATTCTCATATGAGCTTCTCCCTGGTGAAGAAGT 2041
 QY 2041 GAACTGTTACCTTACCTAGAAAGAGAGATACTAGATTCTCTCATGAGGAACTT 2100
 Db 2042 GAACTGTTACCTTACCTAGAAAGAGAGATACTAGATTCTCTCATGAGGAACTT 2101
 QY 2101 GTCCTGCGACAGCATGTCGAAATATCATCACTGCACTGTCAGTCACTGTC 2160
 Db 2102 GTCCTGCGACAGCATGTCGAAATATCATCACTGCACTGTCAGTCACTGTC 2161
 QY 2161 ATCTTGTCTGCTCCACCTTGCCAGTGAGTGGTCCATTAGGACTCTTT 2220
 Db 2162 ATCTTGTCTGCTCCACCTTGCCAGTGAGTGGTCCATTAGGACTCTTT 2221
 QY 2221 GCCATACAACTCTCTCATGAGGACTAACTTAACTCTCTACTGGAAACC 2280
 Db 2222 GCCATACAACTCTCTCATGAGGACTAACTTAACTCTACTGGAAACC 2281
 QY 2281 ATTCACAGACAGCATCCACAGTACAGAGCTGAGGTCTCATGAGGAGCG 2340
 Db 2282 ATTCACAGACAGCATCCACAGTACAGAGCTGAGGTCTCATGAGGAGCG 2341
 QY 2341 ACTTATTGCGAGGCCAAGGAGAAAGCAAACGCTGGCTTTGGCTAACATTAGA 2400

DB	2342	ACTTATTGAGGCCGCCAGGAGAAGCAGCTTTGGCTAACATTAG	2401	Sequence 2760 BP; 850 A; 560 C; 511 G; 838 T; 0 U; 1 Other;
Qy	2401	GCGCTTTAATATGAAATPACACTAGTCAGAAACATGATGTGAATCTAAA	2460	Query Match 99.8%; Score 2748.8; DB 13; Length 2760; Best Local Similarity 99.9%; Pred. No. 0; Matches 2750; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db	2402	GCCGTTTATATGAAATPACACTAGTCAGAAACATGATGTGAATCTAAA	2461	1 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Qy	2461	ATTTAGGAATTCACTAGAACCATATTCTGATGAGATAGTACGT	2520	2 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Db	2462	AATTAGGAATTCACTAGAACCATATTCTGATGAGATAGTACGT	2521	3 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Qy	2521	CCTAGTAACTGTCGGAGCTGCTCCATATCCATGCTCGAGAACACTAACAA	2580	4 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Db	2582	AAACATGTTCACTGGGAACTAGCTGGCTGAGCTGCTGAGAGAC	2641	5 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Qy	2641	AGCCAGCTCTCGGTTAACATATTCTGCTCAATGAACTGCTTGAGAA	2700	6 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Db	2642	AGCCAGCTCTCGGTTAACATATTCTGCTCAATGAACTGCTTGAGAA	2701	7 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Qy	2701	ATGCTCAGTTCTGCTCCTCACTCGCTTCCAAATGCCRTCCTGTG	2753	8 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Db	2702	ATGCTCAGTTCTCCTCACTCGCTTCCAAATGGATCTGTG	2754	9 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
RESULT 6				
ID	ADU23186	standard; cDNA; 2760 BP.		10 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
ID	ADU23186			11 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
AC	ADU23186;			12 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
DT	27-JAN-2005	(first entry)		13 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
DE	Human Toll-like receptor 6 (TLR6)	cDNA sequence - SEQ ID 78.		14 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
KW	screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.			15 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
OS	Homo sapiens.			16 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
PN	WO200404671-A2.			17 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
XX	04-NOV-2004.			18 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
XX	22-APR-2004; 2004WO-US012788.			19 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
XX	22-APR-2003; 2003US-0464586P.			20 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
PR	22-APR-2003; 2003US-0464588P.			21 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
XX	(COLE-) COLEY PHARM GMBH.			22 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
PA	(COLE-) COLEY PHARM GROUP INC.			23 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
XX	Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM;			24 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
DR	WPI; 2004-795573/78.			25 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
PT	Identifying agonists of Toll-like receptor (TLR) signaling activity, useful therapeutically or prophylactically, comprises contacting an RPM8226 cell that expresses a TLR with a test compound and measuring TLR signaling activity.			26 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
PS	Disclosure; SEQ ID NO 78; 342pp; English.			27 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
XX	The invention comprises a screening method for identifying agonists of Toll-like receptor (TLR) signalling activity. The method involves contacting an RPM8226 cell (that expresses a TLR) with a test compound, and measuring a test level of TLR signalling activity, where a test level that is positive is indicative of a test compound that is a TLR agonist. The method of the invention is useful for identifying agonists of TLR. The present nucleic acid represents a TLR cDNA sequence.			28 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Qy	841	ATAGAAAGACTTGAATGCCCTGCTCAGTCCTCAATTCTGCCCCAACCTG	900	29 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Db	842	ATAGAACGACTTGAATGCCCTGCTCAGTCCTCAATTCTGCCCCAACCTG	901	30 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Qy	901	GAATATCTCAATTACATTACATTAATGAAAGTCTGAGAAGATTACT	960	31 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Db	902	GAATATCTCAATTACATTACATTAATGAAAGTCTGAGAAGATTACT	961	32 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Qy	961	TATCTAAACGAGATGAGCTGAGAACATAGACATCTGAGAACAGTCTG	1020	33 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC
Db	962	TATCTAAACGAGATGAGCTGAGAACATAGACATCTGAGAACAGTCTG	1021	34 AGAATTGACTCATCAAGATGCTCGAGAGAACACCCTTAGATGCCACTGC

QY 1021 TTTTCAGAAGACTGTTGACCCGGTTCTGAGATGACATTAGATTTAACATT 1080
Db 1022 TTTCACAGAGCAGCTTGTACACCGTTTGTAGAGATGACATT 1081
QY 1081 TCAGATACACCTTTTACAGATGCTGTTCTGAGATGACATT 1080
Db 1082 TCAGATACACCTTTACAGATGCTGTTCTGAGATGACATT 1081
QY 1141 AACTTACCGAACCTTACAGATGCTGTTCTGAGATGACATT 1140
Db 1142 AACTTACCGAACCTTACAGATGCTGTTCTGAGATGACATT 1141
QY 1201 TTGGAGACACTATCTACAAAAAATGGATAAAGACCTTCAAGTAGGTCTCATG 1200
Db 1202 TTGGAGACACTATCTACAAAGAATGGATAAAGACCTTCAAGTAGGTCTCATG 1201
QY 1261 AGGAAGGATATGCCCTTCTTGAATACTGGATGTTAGCTGGAATCTCTCAAT 1260
Db 1262 AGGAAGGATATGCCCTTCTTGAATACTGGATGTTAGCTGGAATCTCTCAAT 1261
QY 1321 AGACAATAAGAAACTGCACTGGGTGAGGTATGGGTTAAATTGCTCAAT 1320
Db 1322 AGACATAAAGAAACTGCACTGGGTGAGGTATGGGTTAAATTGCTCAAT 1321
QY 1381 ATGCTACTGACTCTGTTAGATGTTACCTCCAGGATCAAGTACTTGATCTCAC 1380
Db 1382 ATGCTACTGACTCTGTTAGATGTTACCTCCAGGATCAAGTACTTGATCTCAC 1381
QY 1441 AGCAATAAAATAAAGAGCTTCTAAACAGCTGTAACCTGGAACCTTGCAAGACTC 1440
Db 1442 AGCAATAAAATAAAGAGCTTCTAAACAGCTGTAACCTGGAACCTTGCAAGACTC 1441
QY 1501 ATATGTCGTTCACTTCACTGACTGACCTCTGGATGTCAGCTGGAACCTTGCAAGACTC 1500
Db 1502 ATATGTCGTTCACTTCACTGACTGACCTCTGGATGTCAGCTGGAACCTTGCAAGACTC 1501
QY 1561 GTATGTCATGTACATCAGTCCCACCATCGGTGATTCAGCTCAGAGCTGC 1620
Db 1562 GTATGTCATGTACATCAGTCCCACCATCGGTGATTCAGCTCAGAGCTGC 1621
QY 1621 CAGAAGATGAGGTCAAAAGCAGGGACATCCATCCATGACTCTGAGCTAAGA 1680
Db 1622 CAGAAGATGAGGTCAAAAGCAGGGACATCCATCCATGACTCTGAGCTAAGA 1681
QY 1681 GAATTGTCAAATAATAGACAGATCAGTGAAGTGTAGGGCTGGCTGATCT 1740
Db 1682 GAATTGTCAAATAATAGACAGATCAGTGAAGTGTAGGGCTGGCTGATCT 1741
QY 1741 TATAAGTGTCACTACCCAGAAGTTAGAGGAAGCCCACTAAAGGACTTCACTGCT 1800
Db 1742 TATAAGTGTCACTACCCAGAAGTTAGAGGAAGCCCACTAAAGGACTTCACTGCT 1801
QY 1801 GAAATTCCGCAACATAACTCTGTCACATCGTGCACCTGTCGACCTGTCGTTG 1850
Db 1802 GAAATTCCGCAACATAACTCTGTCACATCGTGCACATCGTGCACCTGTCGTTG 1851
QY 1861 GCTGTGACTGACCTCCCTCTGGCTACTCTGGATCTGCCCTGGTATCTGGATGG 1920
Db 1862 GCTGTGACTGACCTCCCTCTGGATCTGCCCTGGTATCTGGATGG 1921
QY 1921 TGCCAGTGGACCCAGACTCGGCCAGGGCAGGAACATCCCTAGAGAGACTCAAGA 1980
Db 1922 TGCCAGTGGACCCAGACTCGGCCAGGGCAGGAACATCCCTAGAGAGACTCAAGA 1981
QY 1981 AACCTCCAGTTCTCATGCTTATTCTATGACATGATCTGCTCTGGTGAAGT 2040
Db 1982 AACCTCCAGTTCTCATGCTTATTCTATGACATGATCTGCTCTGGTGAAGT 2041
QY 2041 GAAATTGTCACCTTACCTGAAAGAGATATACGATGTTCTCATGAGGAACTT 2100
Db 2042 GAAATTGTCACCTTACCTGAAAGAGATATACGATGTTCTCATGAGGAACTT 2101
QY 2101 GTCCTCTGGCAAGAGCTTGTGGAAMATATCACTGATGAGAGTACAGTC 2160
Db 2102 GTCCTCTGGCAAGAGCTTGTGGAAMATATCACTGATGAGAGTACAGTC 2161
QY 2161 ATCTTGTGTTGTCCTCAACTTGTGCAAGCTGAGTGGTCCATTAGAACTT 2220
Db 2162 ATCTTGTGTTGTCCTCAACTTGTGCAAGCTGAGTGGTCCATTAGAACTT 2221
QY 2221 GCCCATCACAACTCTTCATGAAAGATCTAACTTAATCTCATCTACTGAAACC 2280
Db 2222 GCCCATCACAACTCTTCATGAAAGATCTAACTTAATCTCATCTACTGAAACC 2281
QY 2281 ATTCCAGAACAGATCCACAGTACAGTACAGTGGCTCTCATGAGCGGG 2340
Db 2282 ATTCCAGAACAGCTTCCACAGTACAGTGGCTCTCATGAGCGGG 2341
QY 2341 ACTTATGTCAGTGCCCCAGGAGAAAGAACCTGCTTGTGCTAACATTGA 2400
Db 2342 ACTTATGTCAGTGCCCCAGGAGAAAGAACCTGCTTGTGCTAACATTGA 2401
QY 2401 GCGCCTTTATGAAATGAACTGACTGACTGAAACATGATGTTGAAATCTCAA 2460
Db 2402 GCGCCTTTATGAAATGAACTGACTGACTGAAACATGATGTTGAAATCTCAA 2461
QY 2461 ATTTAGAAATTCACTAAGAAACCTTAACTGGATGTTGATGTTGACAGT 2520
Db 2462 AATTAGAAATTCACTAAGAAACCTTAACTGGATGTTGACAGT 2521
QY 2521 CGTAAGTACTGTCGGAGGPGCCCATPATCCATGCTCTGGAAAGACTAA 2580
Db 2522 CGTAAGTACTGTCGGAGGPGCCCATPATCCATGCTCTGGAAAGACTAA 2581
QY 2581 AAACATGTTTACATGGGACTCTGAGCTGGCGTGGTTASCTGCGACTGAGAC 2640
Db 2582 AAACATGTTTACATGGGACTCTGAGCTGGCGTGGTTASCTGCGACTGAGAC 2641
QY 2641 AGCCCAAGTCTCTGGTTATCTTATGTTCAATGAAACCTGCTCTTGTGAA 2700
Db 2642 AGCCCAAGTCTCTGGTTATCTTATGTTCAATGAAACCTGCTCTTGTGAA 2701
QY 2701 ATGTCGTTTCTGAGCTCTCCACTCTGCTCTTCCAAATGGATTTG 2753
Db 2702 ATGTCGTTTCTGAGCTCTCCACTCTGCTCTTCCAAATGGATTTG 2754

RESULT 7
AAA39809
AAA39809; standard; CDNA; 2760 BP.
AC
XX
XX
DT 22-SEP-2000 (first entry)
XX
DE Human Toll-like receptor LTR6 cDNA.
XX
XX
XX
XX
XX
OS Homo sapiens.

Key Location/Qualifiers
FT 68..2458
FT /tag= a
FT /product= "TLR6"
XX
PN W020024776-A1.
XX
PD 04-MAY-2000.
XX
PF 26-OCT-1999; 99M0-JP005917.
XX
PR 26-OCT-1998; 98JP-00304110.

PA (NISCC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Akira S., Takeuchi O;

XX PI WPI; 2000-350697/30.

DR P-REDB; AAY88054.

XX PT Toll-like receptor TLR6 molecule and encoded gene, participating in signal transduction of initial immune response, applicable e.g. in PT treating infections.

XX PS Claim 4; Page 25-27; 35PP; Japanese.

This invention describes a novel toll-like receptor TLR6 which has anti-infectious activity. The protein and its encoded gene have clinical use e.g. in treating infections. Toll family receptors are related to transcription factor NF-kappaB and regulate the expression of various genes participating in the immune response. This sequence encodes the human TLR6 protein which is described in the method of the invention

XX Sequence 2760 BP; 850 A; 561 C; 511 G; 837 T; 0 U; 1 Other;

Query Match 99.8%; Score 2747.2; DB 3; Length 2760;
Best Local Similarity 99.9%; Pred. No. 0; Gaps 0;
Matches 2749; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGAATTGGACTCATCAAGATGCTCTGAGAGAACACCTTAGGATGCCACTGC 60
Db 2 AGAATTGGACTCATCAAGATGCTCTGAGAGAACACCTTAGGATGCCACTGC 61
Qy 61 AACATCATGACAAAGCAAGAACCTATGTTAAAGCTCATTTGTGCTTATG 120
Db 62 AACATCATGACAAAGCAAGAACCTATGTTAAAGCTCATTTGTGCTTATG 121
Qy 121 ATCATATAGTGGAACAGATCCAGTCGGAGGAATGAATTGCGTAGACAAG 180
Db 122 ATCATATAGTGGAACAGATCCAGTCGGAGGAATGAATTGCGTAGACAAG 181
Qy 181 TCAAAAGAGGCTTATTCAGTTCCAAAACCTACCGCTGAAACCAAGTCTAGAT 240
Db 182 TCAAAAGAGGCTTATTCAGTTCCAAAACCTACCGCTGAAACCAAGTCTAGAT 241
Qy 241 ATGTCCTGAGACTACATCGCTGAGCTCAGGCTCTGACATGAGCTTCTACAGTTG 300
Db 242 ATGTCCTGAGACTACATCGCTGAGCTCAGGCTCTGACATGAGCTTCTACAGTTG 301
Qy 301 ACAGTTGAGACTTCCATACAGATCAGCTACTGTGTTAAGTGTTCAGTC 360
Db 302 ACAGTTGAGACTTCCATACAGATCAGCTACTGTGTTAAGTGTTCAGTC 361
Qy 361 ACCAGGATTTGAAATCTGATGTTGAGATCTTGTGAAATCTTGTG 420
Db 362 ACCAGGATTTGAAATCTGATGTTGAGATCTTGTGAAATCTTGTG 421
Qy 421 CCTATGTCGAGCTTCAGGATTAGATCTCATTCAGGCTGCATTCAGGCT 480
Db 422 CCTATGTCGAGCTTCAGGATTAGATCTCATTCAGGCTGCATTCAGGCT 481
Qy 481 TGTAGGAAATTGGCAACTTACACATGAAATTCTGGATTGAGTGCATGAAGCTG 540
Db 482 TGTAGGAAATTGGCAACTTACACATGAAATTCTGGATTGAGTGCATGAAGCTG 541
Qy 541 CAAATTAGTGTGCGCCATTGCTCACTGCTTAAGTATATCCTCTGGATTA 600
Db 542 CAAATTAGTGTGCGCCATTGCTCACTGCTTAAGTATATCCTCTGGATTA 601
Qy 601 AGAAATTATAAGAAATGAGCACAAAGTACAAATTGAGCAACAAACC 660
Db 602 AGAAATTATAAAAGAAATGAGCACAAAGTACAAATTGAGCAACAAACC 661
Qy 661 CTCACCTGTGTTCAACCAACTAGTTATGCTATCCAGTGAACATGCTAAT 720
Db 662 CTCACCTGTGTTCAACCAACTAGTTATGCTATCCAGTGAACATGCTAAT 721

Qy 721 ACTTGGGCTTACACTGACTTAAATGATGATGACAACGTCAGTTTC 780

Db 722 ACTTGGGCTTACACTGACTTAAATGATGATGACAACGTCAGTTTC 781

Db 781 ATTAATTTTATGAGACTCACCGAGGGTCAACCTACTGAATTACCTAACAC 840

Qy 841 ATAGAAAGACTTGGAAATGCCCTGAGTCATTTCTAAATTCTGGCCAACCTG 900

Db 842 ATAGAAAGACTTGGAAATGCCCTGAGTCATTTCTAAATTCTGGCCAACCTG 901

Qy 901 GAATTCATATTACAAATGAAAGATTCGGAGAAGATTTC 960

Db 902 GAATTCATATTACAAATGAAAGATTCGGAGAAGATTTC 961

Qy 961 TATTCATAAAGACATTGAGAGACATGACATGAGACATACGAAACAGTTTC 1020

Db 962 TATTCATAAAGACATTGAGAGACATGACATGAGACATACGAAACAGTTTC 1021

Qy 1021 TTTCAGAGACGTTGACCTGTTCTGAGATGACATATGTTAACATT 1080

Db 1022 TTTCAGAGACGTTGACCTGTTCTGAGATGACATATGTTAACATT 1081

Qy 1081 TCAGATCACCTTACATGCTGCTCATGCCAACACTCAAGTTTC 1140

Db 1082 TCAAGATACCTTTATACATGCTGCTCATGCCAACACTCAAGTTTC 1141

Qy 1141 AACTTAACCGAGAACCTTACAGATGAGTTTGAAATAGTTCAGGTTAA 1200

Db 1142 AACTTAACCGAGAACCTTACAGATGAGTTTGAAATAGTTCAGGTTAA 1201

Qy 1201 TTGGAGACACTATCTACAAAAATGGTTAAAGACCTTCAAGTAGCTCAGT 1260

Db 1202 TTGGAGACACTATCTACAAAAATGGTTAAAGACCTTCAAGTAGCTCAGT 1261

Qy 1261 ACCAGGATATGCCCTCTTGAATACTGATGTTGAGATTCTTGTGAACT 1320

Db 1262 ACCAGGATATGCCCTCTTGTGAAATACTGATGTTGAGATTCTTGTGAACT 1321

Qy 1321 AGACATAAGAAACTGCACTGGGTTGAGAGTATAGGGTTAAATGCTCAAT 1380

Db 1322 AGACATAAGAAACTGCACTGGGTTGAGAGTATAGGGTTAAATGCTCAAT 1381

Qy 1381 ATGCTTACATCTGTTGAGTTGAGTTTACCTCCAGGTCAGGTTAGCTGTTAAATGCTCAAT 1440

Db 1382 ATGCTTACATCTGTTGAGTTTACCTCCAGGTCAGGTTAGCTGTTAAATGCTCAAT 1441

Qy 1441 ACCATAATAAGGGCTCTAACAGTCGAACCTGGAGCTTTCAGAACCTC 1500

Db 1442 AGCAATAATAAGGGCTCTAACAGTCGAACCTGGAGCTTTCAGAACCTC 1501

Qy 1501 ATGTCCTTCATCTTAACTGACTGACTCTCTGGATGTTGAGCTTCT 1560

Db 1502 ATGTCCTTCATCTTAACTGACTGACTCTCTGGATGTTGAGCTTCT 1561

Qy 1561 GTATGATCATGATGACAACTGACTTCCACCATCSCGTGTTTCCAGGCTTC 1620

Db 1562 GTATGATCATGATGACAACTGACTTCCACCATCSCGTGTTTCCAGGCTTC 1621

Qy 1621 CAGAGGTGAGGTCAATAAGCAGGACATCCATGCTGAGCTAAG 1680

Db 1622 CAGAGGTGAGGTCAATAAGCAGGACATCCATGCTGAGCTAAG 1681

Qy 1681 GATTTGTCATAAAATAGACCAAGTATGAGTTGAGGGCTGGCTGATCT 1740

Db 1682 GATTTGTCATAAAATAGACCAAGTATGAGTTGAGGGCTGGCTGATCT 1741

Qy 1741 TATAAGTGTGACTACCCAGAGTATAGAGGAACCCACTAAAGCACTTCACATGCT 1800

Db 1742 TATAAGTGTGACTACCCAGAGTATAGAGGAACCCACTTCACATGCT 1801

QY	1801	GAATTACTCTGCAACATAACTCTGCGTCACTCTCACCATCGCGGCCACCATCGCTGGGTGTG	1860	DE Human cDNA encoding an mdrt protein, clone LI:007302.1:2000MAY01.
Db	1802	GAATTACCTCTGCAACATAACTCTGCGTCACTCTCACCATCGCGGCCACCATCGCTGGGTGTG	1861	KW XX Human; molecules for disease detection and treatment; mdrt; ss;
QY	1861	GCTGTGACTCTGCGTCACTCTCACCATCGCGGCCACCATCGCTGGGTGTG	1920	KW Antiarteriosclerotic; hepatotropic; antipsoriatic; cytostatic; immunosuppressive; antidiabetic; antiasthmatic; neuroprotective; osteopathic; antiarrhythmic; arteriosclerosis; cirrhosis; psoriasis; cancer; adenocarcinoma; leukemia; breast cancer; autoimmune disorder; AIDS; acquired immunodeficiency syndrome; Addison's disease; diabetes mellitus; asthma, multiple sclerosis; osteoarthritis.
Db	1862	GCTGTGACTCTGCGTCACTCTCACCATCGCGGCCACCATCGCTGGGTGTG	1921	KW KW
QY	1921	TCCAGTGACCCAGACTCGCGCAGGCCAGAACATACCCCTAGAGATGTTGAGATGTTG	1980	KW
Db	1922	TCCAGTGACCCAGACTCGCGCAGGCCAGAACATACCCCTAGAGATGTTGAGATGTTG	1981	KW
QY	1981	AACTTCGAGTCATGCTTATTCTATGACATGTTCTGCCTGGTGAAGT	2040	KW OS Homo sapiens.
Db	1982	AACTTCGAGTCATGCTTATTCTATGACATGTTCTGCCTGGTGAAGT	2041	KW XX PN WO200162922-A2.
QY	2041	GAATTGCTTACCTTACCTAGAAGAAGATATCAGATTCTCTTATGAGAGAACTT	2100	KW XX PD 30-AUG-2001.
Db	2042	GAATTGCTTACCTTACCTAGAAGAAGATATCAGATTCTCTTATGAGAGAACTT	2101	KW XX PF 21-FEB-2001; 2001WO-US005896.
QY	2101	GTGCCCTGGCAAGAGCATGTCGAAANTATCTACACCTGCGTCAAGTCC	2160	KW XX PR 24-FEB-2000; 2000US-0185213P.
Db	2102	GTGCCCTGGCAAGAGCATGTCGAAANTATCTACACCTGCGTCAAGTCC	2161	KW PR 16-MAY-2000; 2000US-0205332P.
QY	2161	ATCTTGTGTTGTCCTCCAACTTGTTCAGAGTCACTGAGTCACTGTGTT	2220	KW PR 17-MAY-2000; 2000US-0205286P.
Db	2162	ATCTTGTGTTGTCCTCCAACTTGTTCAGAGTCACTGAGTCACTGTGTT	2221	KW PR 17-MAY-2000; 2000US-0205324P.
QY	2221	GCCCCATCACAATCTCTTCATGAGAGCTTAACTTAATCTCACTTACTGGAAACC	2280	KW XX PA (INCY) INCYTE GENOMICS INC.
Db	2222	GCCCCATCACAATCTCTTCATGAGAGCTTAACTTAATCTCACTTACTGGAAACC	2281	KW XX PI Panzer, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC;
QY	2281	ATTCCACAGAACAGCATCCAAACAAAGTACCAACAAGTGAAGGGCTCATGACGCG	2340	PI Chen A, D'sa Sh, Ainsley S, Dahl CR, Dam TC, Daniels SE, Dufour GE; Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL, Liu TF;
Db	2282	ATTCCACAGAACAGCATCCAAACAAAGTACCAACAAGTGAAGGGCTCATGACGCG	2341	PI PI PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W; Cohen RJ, Hodgson DM, Lincoln SE, Jackson S;
QY	2341	ACTTATTGCGTGGCCAAAGAGAAAGAACGTTGGCTCTTGGCTACATTAGA	2400	KW XX DR WPI; 2001-570631/64.
Db	2342	ACTTATTGCGTGGCCAAAGAGAAAGAACGTTGGCTCTTGGCTACATTAGA	2401	KW XX P-PSDB; AAU25469.
QY	2401	GGCGCTTTAAATGAAATTACACTAGTCACTGAAACAAATGATGAAATCTTAAA	2460	KW PT New disease detection and treatment molecule poly nucleotides and polypeptides, useful for diagnosis and treatment of arteriosclerosis, cirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mellitus, PT asthma and multiple sclerosis.
Db	2402	GGCGCTTTAAATGAAATTACACTAGTCACTGAAACAAATGATGAAATCTTAAA	2461	KW PT Claim 1; Page 145; 183pp; English.
QY	2461	ATTAGGAAATCACTAGAACATTATTACTGGATGTTGAAATGAGT	2520	KW CC The invention relates to novel human molecules for disease detection and treatment (mdrt proteins) and the poly nucleotides encoding them. The MDRT poly nucleotides and poly peptides are useful for diagnostic and therapeutic purposes e.g. to diagnose and treat cell proliferative disorders (e.g. arteriosclerosis, cirrhosis and psoriasis) cancers (e.g. adenocarcinoma, leukemia and breast cancer), autoimmune disorders (e.g. acquired immunodeficiency syndrome (AIDS) and Addison's disease), diabetes mellitus, asthma, multiple sclerosis, osteoarthritis, and many more diseases given in the specification. The present sequence encodes an mdrt protein of the invention.
Db	2462	ATTAGGAAATCACTAGAACATTATTACTGGATGTTGAAATGAGT	2521	KW CC Sequence 2940 BP; 898 A; 596 C; 554 G; 892 T; 0 U; 0 Other; XX
QY	2521	CTGAACTGTTCTGGGGACTGAGCTAGCGCGGTGAGGTAGCTGCGGTAGAGAC	2580	KW CC Query Match 99.1%; Score 2727.8; DB 5; Length 2940; Best Local Similarity 99.1%; Pred. No. 0; Matches 2751; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
Db	2522	CTGAACTGTTCTGGGGACTGAGCTAGCGCGGTGAGGTAGCTGCGGTAGAGAC	2581	KW CC 1 AGAAATTGGACTCATATCAGATGCTGAGAGAACACCTTGTAGGATGCCACTGC
QY	2581	AAACAACTGTTCTGGGGACTGAGCTAGCGCGGTGAGGTAGCTGCGGTAGAGAC	2640	KW CC 2 AGAAATTGGACTCATATCAGATGCTGAGAGAACACCTTGTAGGATGCCACTGC
Db	2582	AAACAACTGTTCTGGGGACTGAGCTAGCGCGGTGAGGTAGCTGCGGTAGAGAC	2641	KW CC 61 AACATCATGACCAAGAACAAAGAACCTATGCTAAAGCTCCATTGCTGCTTATG
QY	2641	AGCCCACTGTTCTGGGGACTGAGCTAGCGCGGTGAGGTAGCTGCGGTAGAGAC	2700	KW XX 62 AACATCATGACCAAGAACAAAGAACCTATGCTAAAGCTCCATTGCTGCTTATG
Db	2642	AGCCCACTGTTCTGGGGACTGAGCTAGCGCGGTGAGGTAGCTGCGGTAGAGAC	2701	KW XX 121 ATCATATAGTGGAAACGAGATCCAGGTTCTCCAAATGAGATCTGTTG
RESULT 8	2701	ATGCTCAGTTTCCTCCACTCTCTCTTCCAAATGAGATCTGTTG	2753	KW XX 120
QY	2702	ATGCTCAGTTTCCTCCACTCTCTTCCAAATGAGATCTGTTG	2754	KW XX 121 ATCATATAGTGGAAACGAGATCCAGGTTCTCCAAATGAGATCTGTTG
ID	AAS42521	standard; cDNA; 2940 BP.		KW XX
XX	AAS42521;			
AC	AAS42521;			
DT	18-DEC-2001	(first entry)		
XX				

Qy	181	TCAAAGAGGCTTATCATGTCAAAGACCTACCGCTGAACCAAGTCITAGAT	240
Db	182	TCAAAAGAGGTATTATCATGTCAAAGACCTACCGCTGAACCAAGTCITAGAT	241
Qy	241	ATGCTCAGAATACATGCTGAGCTCAGGCTCTGACATGACTCTCATCAGGTG	300
Db	242	ATGCTCAGAATACATGCTGAGCTCAGGCTCTGACATGACTCTCATCAGGTG	301
Qy	301	ACGTTTGAGACTTCCATACAGAACGATCCAGCTACTGATTAGTGTATCAGGTG	360
Db	302	ACGTTTGAGACTTCCATACAGAACGATCCAGCTACTGATTAGTGTATCAGGTG	361
Qy	361	AACCGAATTAGAACATTGGAATTCTCATAACTGTCACAAAGATACTCCGCCAT	420
Db	362	AACCGGATTAGAACATTGGAATTCTCATAACTGTCACAAAGATACTCCGCCAT	421
Qy	421	CTTATGAGTTCCGGCTTCAAGGCTTAACTGATCTCATTAATGTTCTGAGGTG	480
Db	422	CTTATGAGTTCCGGCTTCAAGGCTTAACTGATCTCATTAATGTTCTGAGGTG	481
Qy	481	TGTAAGGATTTGCAACTTATCACACTGAACTTCTGGATTTGAGTGTCTGAGGTG	540
Db	482	TGTAAGGATTTGCAACTTATCACACTGAACTTCTGGATTTGAGTGTCTGAGGTG	541
Qy	541	CAAAATTAGATTCGCCAATGCTCACTTGCTAAGTATACCTCTGGATTA	600
Db	542	CAAAATTAGATTCGCCAATGCTCACTTGCTAAGTATACCTCTGGATTA	601
Qy	601	AGAAATTATAAAAGAACATGAGCAGAAAGCTACAAATTCTGAATGCAAACC	660
Db	602	AGAAATTATAAAAGAACATGAGCAGAAAGCTACAAATTCTGAATGCAAACC	661
Qy	661	CTTCACCTGTGTTTACCCAACTAGTTATRGCTATCCAAGTGACATACGTTAAT	720
Db	662	CTTCACCTGTGTTTACCCAACTAGTTATRGCTATCCAAGTGACATACGTTAAT	721
Qy	721	ACTTAGGCTTAACTGACTAATAATTGATGATGACAACTGTCAGATTTC	780
Db	722	ACTTAGGCTTAACTGACTAATAATTGATGATGACAACTGTCAGATTTC	781
Qy	781	ATTAATTTTATCAGAACTCACCAAGGAGGTCAACTTACTGATTAACTCTAACAC	840
Db	782	ATTAATTTTATCAGAACTCACCAAGGAGGTCAACTTACTGATTAACTCTAACAC	841
Qy	841	ATAGAACGACTTGGAAATGCCGTTAGAGCTTCAATTCTTGGCCAAACCTGTG	900
Db	842	ATAGAACGACTTGGAAATGCCGTTAGAGCTTCAATTCTTGGCCAAACCTGTG	901
Qy	901	GAATCTCAATTACAATTAACATAATTGAAAGCATCTGAGAGATTACT	960
Db	902	GAATCTCAATTACAATTAACATAATTGAAAGCATCTGAGAGATTACT	961
Qy	961	TATCTAAACGACATGAAAGCTTACAATAGAACATATCAGAACCTTTCTG	1020
Db	962	TATCTAAACGACATGAAAGCTTACAATAGAACATATCAGAACCTTTCTG	1021
Qy	1021	TTTCAAGACAGCTTGTACACCGTTCTGAGTAGATTATGAGCTAACATT	1080
Db	1022	TTTCAAGACAGCTTGTACACCGTTCTGAGTAGATTATGAGCTAACATT	1081
Qy	1081	TCTGATGACCTTACACATGCTGCTCTCATGCCAACCATCAGTTTG	1140
Db	1082	TCTGATGACCTTACACATGCTGCTCTCATGCCAACCATCAGTTTG	1141
Qy	1141	AACTTACCCAGACGTTCAAGATGTTGAGTATTTGAAAATGTCACCGTTAGTTAA	1200
Db	1142	AACTTACCCAGACGTTCAAGATGTTGAGTATTTGAAAATGTCACCGTTAGTTAA	1201
Qy	1201	TGGAGACACTTACATCAAAAAAGGTTAAACACCTTCTCAAGTAGGTCTCATG	1260
Db	1202	TGGAGACACTTACATCAAAAAAGGTTAAACACCTTCTCAAGTAGGTCTCATG	1261

CC SEQ ID NO 1829 are provided.
 XX
 SQ Sequence 2391 BP; 742 A; 485 C; 436 G; 728 T; 0 U; 0 Other;
 Query Match 86.9%; Score 2391; DB 14; Length 2391;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2391; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 2341 ACTTATTGCGCTGGCCAAGGAAANACCAACT-GGGCTTTGGGTACATAG 2399
 Db 2342 ACTTATTGCGCTGGCCAAGGAAANACCAACT-GGGCTTTGGGTACATAG 2401

QY 2400 AGCGCCTTTAATATGAATAACTAGTCACTGAAACAACTGATGTAACCTAAA 2459
 Db 2402 AGCGCCTTTAATATGAATAACTAGTCACTGAAACAACTGATGTAACCTAAA 2461

QY 2460 AAATTAGGAATTCAACTAGAACCATTTACTTGATGATGTGATAGTACAG 2519
 Db 2462 AAATTAGGAATTCAACTAGAACCATTTACTTGATGATGTGATAGTACAG 2521

QY 2520 TCGTAAGTAACTGTCGGAGCTGCCTCATATTCATGCTCAGGAAGACTRACA 2579
 Db 2522 TCGTAAGTAACTGTCGGAGCTGCCTCATATTCATGCTCAGGAAGACTRACA 2581

QY 2580 AAACAACTGTTCACTCTGGGAACTTAACTTGATGAGCTGGCTAGGTTAGAGA 2639
 Db 2582 AAACAACTGTTCACTCTGGGAACTTAACTTGATGAGCTGGCTAGGTTAGAGA 2641

QY 2640 CAGCCAGTCTCTCGTTATCATATTTCAATT-GAACAGTCTTTGAGT 2698
 Db 2642 CAGCCAGTCTCTCGTTATCATATTTCAATT-GAACAGTCTTTGAGT 2701

QY 2699 AAATGCTCAGTTCACTCTCACTCTGCTTCCCATAATGGATCTGTG 2753
 Db 2702 AAATGCTCAGTTCACTCTCACTCTGCTTCCCATAATGGATCTGTG 2756

RESULT 9
 ADV2616
 ID ADV2616 Standard; cDNA; 2391 BP.

XX ADV2616;
 AC
 XX DT 10-MAR-2005 (first entry)

DE Human psychoneuroendocrine expressed sequence tag SEQ ID NO 244.

XX microarray; psychoneuroendocrine; chronic fatigue; KW non-insulin dependent diabetes; allergy; immune disorder; inflammation; KW cancer; neoplasm; infection; expressed sequence tag; ss; KW Homo sapiens.

XX WO2004108899-A2.

PD 16-DEC-2004.

XX 04-JUN-2004; 2004WO-US017686.

XX 04-JUN-2003; 2003US-0475915P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Nicholson A, Vernon SD;
 PI
 XX WPI; 2005-031682/03.

XX PT New microarray comprising probes for genes involved in psychoneuroendocrine (PNI) activity, useful in diagnosing a condition associated with PNI activity, e.g., inflammatory or infectious diseases.

PS Claim 1; SEQ ID NO 244; 254pp; English.

XX
 CC The invention relates to a new microarray which comprises probes for genes involved in psychoneuroendocrine (PNI) activity. The microarray is useful in diagnosing a condition associated with PNI activity, such as, type-2 diabetes, allergic condition, inflammation, cancer and infection. The present sequence represents a psychoneuroendocrine gene expressed sequence tag. Note the specificatio mentions SEQ ID No of up to 3314 but only sequences up to

CC SEQ ID NO 1829 are provided.
 XX
 SQ Sequence 2391 BP; 742 A; 485 C; 436 G; 728 T; 0 U; 0 Other;
 Query Match 86.9%; Score 2391; DB 14; Length 2391;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2391; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 67 ATGACCAAAGACAAGAACCTTATGTTAAAGCTTCCATTGTTGCCATTGATCTATA 126
 Db 1 ATGACCAAAGACAAGAACCTTATGTTAAAGCTTCCATTGTTGCCATTGATCTATA 60

QY 127 ATAGTCGACCGAGAACTTCCAGITCTCCGACGGAAATGATTGCGTAGAAGTCMAA 186
 Db 61 ATAGTCGACCGAGAACTTCCAGITCTCCGACGGAAATGATTGCGTAGAAGTCMAA 120

QY 187 AGAGGTTTATTCATGTTCCAAAGAACCTACCGCTAAACCAAACTGTTAGATGTCT 246
 Db 121 AGAGGTTTATTCATGTTCCAAAGAACCTACCGCTAAACCAAACTGTTAGATGTCT 180

QY 247 CAGAACTACATGCGTGTAGCTTCAGGTTCTGACATGAGCTTCTATCAGCTGTGAGTT 306
 Db 181 CAGAACTACATGCGTGTAGCTTCAGGTTCTGACATGAGCTTCTATCAGCTGTGAGTT 240

QY 307 TTGAGACTTCCATACAGATCCGCTACTGTTAGTTAGTAACTGTTCAACAG 366
 Db 241 TTGAGACTTCCATACAGATCCGCTACTGTTAGTAACTGTTCAACAG 300

QY 367 GATTTAGAATTTGTTATTCATATAGTGGCAAAAGATACTCTSCATCTATT 426
 Db 301 GATTTAGAATTTGTTATTCATATAGTGGCAAAAGATACTCTSCATCTATT 360

QY 427 GTGAGTTTCAGGATTAGACTCTCATTCATGTTCAAGGCCCTGCCATCTGTAG 486
 Db 361 GTGAGTTTCAGGATTAGACTCTCATTCATGTTCAAGGCCCTGCCATCTGTAG 420

QY 487 GAATTGCGAACTTACACAGTAACTGAAATTCTGGATGAGCTGCTATGAGCTGCAA 546
 Db 421 GAATTGCGAACTTACACAGTAACTGAAATTCTGGATGAGCTGCTATGAGCTGCAA 480

QY 547 TTAGATTGCGCAATTGCTCACTGCTACTGCTCATCTAGTTCAAGGCCCTGCCATCTGTAG 606
 Db 481 TTAGATTGCGCAATTGCTCACTGCTACTGCTCATCTAGTTCAAGGCCCTGCCATCTGTAG 540

QY 607 TATTATTAAGAGAAATGAGACAGAAAGTCAATTCTGAATGCAAACCTCTAC 666
 Db 541 TATTATTAAGAGAAATGAGACAGAAAGTCAATTCTGAATGCAAACCTCTAC 600

QY 667 CTGTTTCAACCAACTAGTTATCGCTATCCAACTGACATCTGTTAACTTTA 726
 Db 601 CTGTTTCAACCAACTAGTTATCGCTATCCAACTGACATCTGTTAACTTTA 660

QY 727 GGGTGCCTACACTGACTGAAATTATGATGATGACACTGCAAGTTCTAA 786
 Db 661 GGTTGCTTACACTGACTGAAATTATGATGATGACACTGCAAGTTCTAA 720

QY 787 TTTTATCAGACTCACAGAGTTCAACCTACTGAAATTCTACCCACATAGA 846
 Db 721 TTTTATCAGACTCACAGAGTTCAACCTACTGAAATTCTACCCACATAGA 780

QY 847 AGCACTGGAAATGCTGGTAGCTTCATTCCTGGCCAAACCTGTGGATA 906
 Db 781 AGCACTGGAAATGCTGGTAGCTTCATTCCTGGCCAAACCTGTGGATA 840

Db 907 CTCATAATTACAAATTACAAATTGAAAGCATCTGGAAAGAGTTTACTTCT 966

QY 841 CTCATAATTACAAATTACAAATTGAAAGCATCTGGAAAGAGTTTACTTCT 900

QY 967 AAAACGACATGAAAGCATCTGGAAAGCATCTGGAAAGAGTTTACTTCT 1026
 Db 901 AAAACGACATGAAAGCATCTGGAAAGCATCTGGAAAGAGTTTACTTCT 960

QY 1027 CAGACAGCTTGTACACCGCTGTTCTGAGATGACATATGAGCTTACCTTCAGAT 1086

Query	Match	Score	DB	Length
Qy	55.7%; Score 1533.6; DB 3; Length 2604;			
Matches 1930; Conservative 0; Mismatches 596; Indels 10; Gaps 3;				
Db	4 TCAAGATCTCTGAAGAAGAACACCCATTGGATAGCCACACATGACCAAG	76	1024 TATACTCGGTGTTGGAGTCAACATCTGCTCTCAGACACCCATTCA	1083
Qy	77 ACAAGAACCTAATGTTAAAGCTTCATTTRTGTTCTATGATCATATAGTCAAAG	136	1097 TACACATGCTGTCCTCATGGACACAGCACATCAAGTTGAACCTACCGAGAC	1156
Db	64 ACAGAAACCCATCTGGTGGGAGTTCCACTTCTTGCCTTGCCUTATAGTCGAA	123	1084 TCCACATGGTGGCCACATCCCAAGCTCTTACATTCTGACATTACCGAG	1143
Qy	137 CCGAATCCAGITCTCCAGGAATGATTGAGTCAGTAGACAGTCAGAACAGGCTTA	196	1157 TTTCACAGATGATTGAAAGTTCACAGTTAGTAATGGAGACACTATCT	1216
Db	124 GEATGACCCGTTCTTAATGACTTGAGTCTATGGAGACATTCACAGGAACTTA	183	1144 TTTCACAGTGTTCAGGCTGTCACCTTAAGGATGAGACTT	1203
Qy	197 TCTATGTTCCAAGAACCTAACCCGCTGAAACCAAGCTTAAATGTTGAA	256	1217 TACAAAAAATGGATTAAGACCTTCAAGTAGCTATGAGCAAGGATATCCT	1275
Db	184 CTATGTCGCCAAGACCTGCCCCAAGAACAGAACAGAACAGAACACTTA	243	1204 TACAAGAATGTTTAAGACTGACTCTCATGACTAAGATAATGCT	1263
Qy	257 TGGCTGAGCTCAAGTCAGGTCTCTGACATGAGCTTCTATGAGTTGAGCTT	316	1277 CTTGGAATACTGGATGTTAGCTGGATCTGGATCTGGATCTGGACATAAGAAACT	1336
Db	244 TATCTGAGCTTGATGCTGCTGATACAGCTTCTGTCAGAGCTGAGACTCT	303	1324 GGCCCTGGCTGAGGAGATATGGTGTGTTGACTCATGATAGTCAGGCTG	1383
Qy	317 CCCATAACAGAACTCCAGCTACTGATTAAGTTCAAGTCACCGAGGTTGAI	376	1264 CTCGGAACTTGGATGTTAGTTGACTCATGATAGTCAGGACAT	1323
Db	304 CCACACAGGATACGGAGCTGATGTTCCATGTTCTGTTCACTCAGGACTTA	363	1397 TTTCAGATGTTACTCCGGATAGGACTGATCTCACGCCATAATAAGA	1455
Qy	377 ATTGGATTATCTCATATCAGTTGCAAAAGATATCTGCCATCTTGGAGTTCA	436	1337 CTTAACAGGTTGAGAGTAACTGGCTTAATTTGCTCAATATGCTACTG	1396
Db	364 ACCGGGTTCTCACACATCGCTGCTGCTGCTGCTGCTGCTGCTG	423	1204 TCTTCAGATGTTACCTCCAGGTCAGGTTCACTTCACACACAGGAT	1443
Qy	437 CGCATTTGAGCTCTCATTCATGATTCAGGCTGCCATCTGAAAGGATTGCA	496	1457 GGTTCCAAACAGTGTAAACTGGAGCTTGGAAGACTCACAGTGTCTTCA	1516
Db	484 ACCTGAGAACTGACTTCTGGATAAATGCTGCAAAATGGCAATGGCTGC	543	1504 CCTTAACCTGACCTTCCTGGTGTGGGGCTTCAGCAGCCTTCIGCTGGTCATGCC	1563
Db	424 GGCATCTAGACCTCTCATCTGACTGACTTGCTCTGTTAGGAAATTGGA	483	1577 ACAATTCAAGTTCACCTGCTCATCTGGCTGTTCTCAGAGATGAGCTCAA	1636
Qy	497 ACTTATCACACTGAATTCTGGATGATGCTCTGAACTGCAAATAAGATTG	556	1517 CTTAACAGCTCTCTGGATGCTGAGCTTCTGAGCTTCTGATCATGTC	1576
Db	444 ATCTGAGAACTGACTTCTGGATAAATGCTGCAAAATGGCAATGGCTGC	543	1564 ATAACTGATGTTCCATCCCTCTGAGATTTCTCAGASCTGTCAGAAATTGATCA	1623
Db	557 TCGCAATGTCACTGTCATTAAGTTATATCTCTGGATTAAGAAATTATATAA	616	1637 TAAAGGAGGACATTCATCCAACTGTTGAGCTAAAGAAATTGTCAAATA	1696
Db	544 TCCAGTTGCTACTCTCATGCTCATCTCTGGCTGAGTAGTGTATCATATAA	603	1624 TACAGGGAAACACCCATCCATGTCAGCTGAGCTGAGGACTTCTGAGA	1683
Qy	617 AGAAAAATGACACAGAAAGTCTACAATTCTGATGAACTATGTTAACTTTGGGTTAC	676	1697 TAGACCAAGTACAGGAACTGGGCTGCTGTTCTATAGTGACTAC	1756
Db	604 AAGGGGGGAAACAGAAAGTCCTGAGATCCACACCGCTTCATGTTCTC	663	1684 TAGGCTGGTAGCAAGGAAGTGGGGAGGGCTGSCCTGACTCTACGGGTTAC	1743
Qy	677 ACCCAACTAGTTATGGCTATCACAATTCTGATGAACTATGTTAACTTTGGGTTAC	736	1757 CAGAAAGTTAGAGGAGGCCACTAAAGGACTTTCACATCTGTTGAACTGCA	1816
Db	664 ATCCAAATAGCTGTCCTGTCAGTAAACGCTTACGATGAACTGAGCTTAC	723	1744 CAGAAAGCTCTGGAGGACTGCACTGGGGACTTCCACATGTCCTGACTA	1803
Qy	737 ACTGACTAATTAATGAGATGACAACACTGTCAGTTCTATTTTACAG	796	1817 TAATCTGCTGTCAGTACCTGGCCACCATGGGGACTATGTTGGCTGACTGTCAC	1876
Db	724 ACTGACTAATTAATGAGATGACAACACTGTCAGTTCTATTTTACAG	783	1804 CTGTTCTGCTGACTGCACTGGCCACATGGGGACTATGTTGGCTGACTGTCAC	1863
Qy	797 ACTCTCAGGAGGTCAACCTTACCTGATTCACCTCAACACATAGAAAGACTG	856	1877 CCCTCTGCTACTTGATGCTCTGGATCTCAGATGTTGCTGCACTGGACCGA	1936
Db	784 AACCTCAGGAGGTTCAACTTTCTGACCTTATGGATGAGCTCCACACAGGAACTG	843	1864 TCTCTCTCTACTTGACCTGCTGCTGGTATGAGGATCTGTCAGGACAGA	1923
Qy	917 ACATTTACAAATATGAAACCATGGAGAGATTACTTATCTAAACACAT	976	1937 CTGGCCAGGCCAGAACATACCTTCTGAGAACTCAAAACTCCAGTTCT	1996
Db	904 ACACATTACAACTAACTGGAGAATGCAAGGGAAAGTACTCTGGAGACGAC	963	1924 CCAGGCAAGGCCAGCACATCCCTCTAGAGAACTCCAGTCAGTCATG	1983
Qy	957 AATGCCCTGGTAGAGCTTCAATTCTGGCCCAACCTGGAATATCTAAATT	916	1997 CTTTCATATGAGCTGAGATGTTCTGCTGCTGGTGAAGTGAATGTTGCTTAC	2056
Db	844 AGTGCCTGGTTAACTTTCTCAATTCTGGCCGACGGTGGAGTACCTCAATT	903	1984 CTTTCATACAGTGGCTGCTGGTGAAGGACCTTACCTACCA	2043
Qy	917 ACATTTACAAATATGAAACCATGGAGAGATTACTTATCTAAACACAT	976	2057 TAGAAAGAGAGATAACAGTTGCTCTGAGAGAACTTCTGGCAAGAGCA	2116
Db	904 ACACATTACAACTAACTGGAGAATGCAAGGGAAAGTACTCTGGAGACGAC	963	2044 TAGAGAGATGACATCCGGTTGCTCCATGAGAGAACTTCTGGCAAGAGCA	2103
Qy	977 TGAAGGATTGACAACTGACATATGAGGAACTTCTGGTTCAGAGACGTT	1036	2117 TTGTGAAATATCATCAACTGCTGAGAGAGTTCAAGTCCTCTTGTCTC	2176
	1037 TGTACACCGGTTTCTGAGATGACATTATGATGTTAACCATTCAGATCACCTTTA	1096		

Db	2104	TGTGGAGACATCATCAATTCTATGAGAAGGTTACAGGCCATCTTGTGCCTTC	2163	CC The present nucleic acid represents a TLR cDNA sequence.
Qy	2177	CCA CTT GTG TCA GAG TG AGT GTG TGC ATT GA A CT C T A T G C C A T C A A T C T C T	2236	CC Sequence 2604 BP; 689 A; 615 C; 561 G; 739 T; 0 U; 0 Other;
Db	2164	CC C A C T C A T C A T C A G A G T G A G G T G T G C A T T G A A C T C T A T T T G C C A T Q T A A T C T C T	2223	SQ Query Match: Best Local Similarity 55.7%; Score 1533.6.; DB 13; Length 2604; Matches 1930; Conservative 0; Mismatches 596; Indels 10; Gaps 3;
Qy	2237	TTC AT G A G A G T C T A A T A C T T A A T C T C A C T T A C T G A A C C A T C C A C C A G A C A G C A	2296	Qy 4 TA A A T G C T G A M A G A T G T A A N G T C C T C A T G A C G C R O G G A C T A T T G C A G T G C C
Db	2224	T C C A T G A A G G C T C T G A T C H T A C T T A C T C A T C T G C G A C A T C A G C A A A G	2283	Db 77 A C A A G A C C T A T G T T A A A G C T C T C A T G A C T G C C A T T G G A A G C T T A G C C A C T G C A A G 76
Qy	2297	T T C C C A A C A A G T A C C A C A G G T G A A G G C T C T C A T G A C G C R O G G A C T A T T G C A G T G C C	2356	Qy 64 A C A G A A A C C A T C G C G G A G G T T C C A C T T G T G T G C G C C T T G C C T T A T A G T C G G A A 123
Db	2284	T T C C C A G T A G A T T A C C A C A G G T G C G G G C T C T C A T G A C G C R O G G A C T A T T G C A G T G C C	2343	Qy 137 C C A G A T T C A S T T C C G A C G G A A M T G A A T T G C A G T G A C T G A C A G T C A M A A G A G G T T A 196
Qy	2357	C C A G G A A A A G C A A C G T G C T C T T G G C T A C A T T A G A G C G C T T A A T A T G A	2416	Db 124 G C A T G A C C C G G T C T C A T G A A C T G G A I C T G A G I T G A C A G T C A A C A G G A C T T A 183
Db	2344	C T A C T G A G A G C G C A A C G T G C G C T T G G C C A C C T T A G A G C T T C A T T A T A T G A	2403	Qy 197 T T C A G T G C T C C A A A C T C A C C T A C C G C T G A A A C C A A G T C T T A G A T G T C T C A G A C T A 256
Qy	2417	A T T A C A C T G T C A X T G A A C A M T G A T G T G A A T T T A A A A T T G G A A M T C A A	2476	Db 184 C T C A T C T C C A A A G C A C T G C C A C C A A G C A A A G C C T G A G T C T G T C T C A A A C T A 243
Db	2404	A G T T A G C C T C T A G T C A M G -- A G G A T G T G A A R A C T T G A A -- C T T G G T T C T C A A	2456	Qy 257 T G C T G A G C T C A G E T T C G A T G A C T G A G C T T C A G T H A T G T G A G C T T 316
Qy	2477	C T T A G A A C C A T T A T T A C T T G A T G T C A T G T G A A T G A T A G T C A G T C G T A G T A C T G	2536	Db 244 T A T C T G A C T T G C C T G A T A C G C T G A G C T G A G G T C T G A G A C T A 303
Db	2457	C T T A A T A A C C -- T G T C A A C T G G G T T C A T G A A C T G G T T C A G T T C C T C A C T G	2513	Qy 317 C C C A T A C A G A T C C A G G A C T A T G T G A T T A A G T G T T C A G T C A C C A G G A T T A A T 376
RESULT 1				Db 304 C C A C C A C A G A T A G G A G C T T C A T G H A T T C T G T G C A T C A G G A T T T G C A 363
ADU23191	ID	ADU23191 standard; cDNA; 2604 BP.		Qy 317 A T T T G G A T T A A T C T C A T T A A T C A T G T G C A A A A G A T A T C C T C C A T C T A T G T G A T T C A 436
XX	AC	ADU23191;		Db 364 A C C T G G A T G T C T C A C A C A T C G G T T C C A A A C A T C T C T C T C T C G C C T A T G C G A G C C T G A 423
XX	DT	27-JAN-2005 (first entry)		Qy 437 G G C A T T P A G A R T C T C A T C A T G A T T C A A G G C C T C G C C A T C T G T A M G G A T T T G G C A 496
XX	DE	Murine Toll-like receptor 6 (TLR6) cDNA sequence - SEQ ID 83.		Db 424 G G C A T C H A G A C C T C T C A T C A T G A T T C A T G T A G T A C T G C C T G T G T A A G G A T T T G G C A 483
XX	KW	screening; Toll-like receptor agonist; TIR agonist; gene; ss; TLR6.		Qy 497 A C T T A T C A C A C T G A T T C T C T G G A T T G A G G T C T A G G C T G T A T G A G C T G C G A A A M A T T A G T T C 556
OS	Mus sp.			Db 484 A C C T G A C G A A G C T G A C T T C T G C G A T T T A A G G A T T T G G A T T A A G A A T T A T T A A 543
XX	PN	WO2004094671-A2.		Qy 557 T G C C A M T G C T C A C T G C A T C T A A G T T A M T C C T C T G G A T T A A G A A T T A T T A A 616
PD	04-NOV-2004.			Db 544 T C C C A G T G C T C A C T G C A T C T A A G T G C A T T C T G G A T T A A G G A T T T G G A T T A A 603
XX	PP	22-APR-2004; 2004WO-US012788.		Qy 617 A A G A A A T T A G A C A G A G A T C T A C A A A T T C T G A M G C A A A A C C T T C A C T T G T T T C 676
XX	PR	22-APR-2003; 2003US-0464586P.		Db 604 A A G G G G G A A C A C G A A G T C T C A G A T T C C A A T A C C A C G G T T C T C A T T G G T T C 663
PR	22-APR-2003; 2003US-0464588P.			Qy 677 A C C C A T G A T T C T G C T A C T C A T C A T G A C A T T A A T C T T A G G G T G C T A C 736
XX	PA	(COLE-) COLEY PHARM GMBH. (COLE-) COLEY PHARM GROUP INC.		Db 664 A T C C A M A S C T G T C T C T C A G T G A C A T G T C T G A A C C T T G C C T T A G G A T T A 723
PA	PI	Volmer J., Juzk M., Lipford GB, Schetter C, Forsbach A, Krieg AM;		Qy 737 A A C T G A C T A A T T A A T T G A T G A C A C T G T C A G T T C T C A G T G A C A T G T C T G A A C T T C T G A 796
XX	DR	WPI; 2004-795573/78.		Db 724 A A C T G A C T A A T T A A T T G A T G A C A C T G T C T G A C T G A A C T T G C T G A A C T T C T G A 783
XX	PT	Identifying agonists of Toll-like receptor (TLR) signaling activity, useful therapeutically or prophylactically, comprises contacting an RPMI8226 cell (that expresses a TLR) with a test compound, and measuring a test level of TLR signalling activity, where a test level that is positive is indicative of a test compound that is a TLR agonist.		Qy 797 A A C T C A C C A G G T T C A C C T T A C T G A T T T A C C C T C A C C A T A G A A C G A C T T G G A 856
CC	CC	The invention comprises a screening method for identifying agonists of Toll-like receptor (TLR) signalling activity. The method involves contacting an RPMI8226 cell (that expresses a TLR) with a test compound, and measuring a test level of TLR signalling activity, where a test level that is positive is indicative of a test compound that is a TLR agonist.		Db 784 A A C T C A C C A G G T T C A C C T T A C T G A T T T A C C C T C A C C A T A G A A C A C T G G A 843
CC	PS	Disclosure; SEQ ID NO 83; 342bp; English.		Qy 857 A A T G C T G G T C A G A G T T C T C A A T T C T T G C C C A A C C T G T G C A A T T C T C A T A T T 916
XX	PS			Db 844 A G T G C T G G T T A A C T T C T C A T T C T T G C C C G A C C G G T G A G T C T C A A T T 903
CC	CC			Qy 917 A C A T T A C A T A T T G A M G C A T T G G A A G A T T A C T T C T A A A G C A T 976
CC	CC			Db 904 A C A C T A C G A T A C T G A G A G C A C G G A A G T T A C T T C T C G G A G A C 963

QY	977	TGAAGGATTGACAATGAACTATCACGACCAAGTTTCTGTTTCAGACAGCTT	1036	Db	2044			TAGAGAAGATGACATCGGGTTGCCATGAGGAACTTGTCCCTGCGAAGCA	2103		
Db	964	TCAAGTCACTGATGAGACAGCTCAAAGGAGGC	1023	QY	1037	TGTACACCGTGTTCAGAGTAACTATAGTTAACATTAGATACTGACCTTTA	1096	2117	TGTTGAAATCATCCTACTCATGAGAGAGTTCAAGTCCATTTTGCTC	2176	
QY	1024	TATACCTGGTTGCTGAGATGAACTTACAGTCAGTCACTCTGAGACCTTA	1083	Db	2104	TGTGGAACTCATTCATGAGAGTTTCAAGTAACTGACCTTCTC	2163	TTGTTGAGAACTCATTCATGAGAGTTTCAAGTAACTGACCTTCTC	2163		
Db	1097	TACACATGCTGTCATGAGACCTTACAGTCAGTTGAACTTACCTTAC	1156	QY	1084	TCCACATGGTGGCCCATGCCAACGCTTACATTCTGAACCTTAC	1143	2117	CCAACTTGTCAGAGTGAGTGTGCACTTACAGTAACTTACCCAGAC	2236	
QY	1144	TTTTACTGAGATGTTTACAGTCAGTTTACAGTCAGTTTCAAGTAACTTAC	1203	Db	2164	CCACCTCATCCAGAGTGAGTGTGCACTTACAGTAACTTAC	2223	TTCCACAAAGTACCGAGCTGAGGCTCTCATGAGCAGGACTTATGAGGC	2356		
Db	1217	TACAAAAAAATGATTAACACCTTCAAAAGTAGTAGTCTCATGAGAAGGATATGCTT	1276	QY	1204	TACAAAGGAAAGTTTAAAGACTTTAAAGTCTTAAAGTAGCTGAGAATGCT	1263	2237	TTCATGAGGTTCTAACTTAATGAGTCTCATGACTAAGAATGCT	2296	
QY	1277	CITGGAAATCTGAGTTTACAGTCAGTTTACAGTCAGTTTAAAGAGAACT	1336	Db	2224	TCCATGAGGCTGTGAACTTAATCTCATGAGCAGGACTTATGAGGC	2283	CCAACTTGTCAGAGTGAGTGTGCACTTACAGTAACTTACAGAACA	2283		
Db	1264	CCTGGAACCTTGGATTTGACTTGTGAACTTACAGTCAGTTTCAAGGACAT	1323	QY	1337	CACTTGGTTGAGAGTATGGTTAAATTGTCCTCAATATGCTACTGCTG	1396	2297	TTCCACAAAGTACCGAGCTGAGGCTCTCATGAGCAGGACTTATGAGGC	2343	
QY	1324	GCGCCCTGGCTGAGACATATGTTGTTCAATAGCTTACAGGCT	1383	Db	2284	TCATGAGGTTTACCCAGGATCAGGTTACTTGTGAACTTACAGTCA	2403	TCACCTGAGTATACCACAGGCTGCGGCTCTCATGAGCAGGGACTTACTGG	2343		
Db	1397	TTTCAGATGTTACCTCCAGGATCAGGTTACTTGTGAACTTACAGTCA	1456	QY	1384	TCTTCAAGTGTACTCCAGGTCAGGTTCTGAGGACTTACAGTCA	1443	2417	AATTAACACTGACTGAAACATGATGAACTTAAAATTTGAAATTAA	2476	
QY	1457	CGGTCTTAACAAAGCTGTAACATCGAGGTTGEGAGACTCAATGTTCAATT	1516	Db	2404	AGTTAGCTTGTCAAGT--AGGATGATGGAAGACTTGAA---CTTGGTTCTAA	2456	CCAAAGGAAAGCAGTCAGGGCTTTCGGCTCTGGCCACCTAGAGCTTATGAA	2456		
Db	1444	GCATCCTAAAGATGTCACCCACCTGAGGTTGAGGAACTCAACAGGATATG	1503	QY	1517	CTTAACTGACCTCTGGATGGAGCTTCTGAGGTTCTGATGATCATGTC	1576	2477	CTTAAAGAACATTATTACTTGTGATGGTGAATGAGTACAGTCGTTAGTCTG	2536	
QY	1504	CCTTAACTGACTCTCTGGGCTTCTGAGGTTCTGAGGTTCTGAGGTTCTG	1563	Db	2457	CTTAATPAC---TGCACCTGGGCTCTGAGACACTGCGGTTTACGTTACTG	2513	CTTAAAGAACATTATTACTTGTGATGGTGAATGAGTACAGTCGTTAGTCTG	2513		
Db	1577	ACAACTGAGTTCCACCATGGCTGATTCTCCAGAGGCGCCATGAGGCTAA	1636	QY	1564	ATTAACCTGAGTTCCGATCCTCTGAGGTTCTGAGGTTCTGAGGATATGCTCC	1623	2537	GAGGCTCTCCATTATGAGGTTCTGAGGAACTGCGGTTTACGTTACTG	2552	
QY	1637	TAACACGGGAAACACCATCCAAATGAGGAACTTACAGGAA	1696	Db	2514	GAGGTTCTCTGTTGAGGAACTGCGGTTTACGTTACTG	2529	2514 GAGGTTCTCTGTTGAGGAACTGCGGTTTACGTTACTG	2529		
Db	1624	TAACACGGGAAACACCATCCAAATGAGGAACTTACAGGAA	1683	RESULT 12							
QY	1697	TAGACCAAGAGTCAGTGAAGTGTAGAGGGCTGGCTGATCTATAAGGTGACTAC	1756	ADU23192	ADU23192	ADU23192	ADU23192	ADU23192	ADU23192	ADU23192	ADU23192
Db	1684	TAGGCTGGTGTGAGGAGAGTGGTGTGAGGCTGCTGACTCTACAGGGTGTGACTAC	1743	XX	XX	XX	XX	XX	XX	XX	XX
QY	1757	CAGAAAGTTATAGAGGAAAGCCACTAAAGGCTTACATGATCTGATTATGCAAA	1816	XX	XX	XX	XX	XX	XX	XX	XX
Db	1744	CAGAACGCTCTAAGGAACTGACTGACCTGCTGACTGCTGACTGCTGACTG	1803	XX	XX	XX	XX	XX	XX	XX	XX
QY	1817	TAACTCTGCTGTATGTCACCTCGGGCCACATGCTGTTGCTGACTGACT	1876	XX	XX	XX	XX	XX	XX	XX	XX
Db	1804	CTGTCCTGCTGCTACTGTCACCTCGGGCCACATGCTGTTGCTGACTGGGTT	1863	XX	XX	XX	XX	XX	XX	XX	XX
QY	1877	CCCTCTGCACTACTGATGCTGCCCTGGATCTCGGATGTTGCCAGTGGACCCA	1936	XX	XX	XX	XX	XX	XX	XX	XX
Db	1864	TCTCTGCTGCTACTTGACTGCTGCCCTGGATGTTGCCAGTGGACCCA	1923	XX	XX	XX	XX	XX	XX	XX	XX
QY	1937	CTCGGGCAGGCCAGGAACCTACCCCTAGAGAACTCCCAAAGAACCTCGAGTTG	1996	XX	XX	XX	XX	XX	XX	XX	XX
Db	1924	CCAGGACAGGCCAGGACACTCCCTAGGAAACTCCCAAAGAACCTCGAGTTG	1983	WPI; 2004-795573/78.	(COLE-)	COLEY PHARM GMBH	(COLE-)	COLEY PHARM GMBH	(COLE-)	COLEY PHARM GMBH	(COLE-)
QY	1997	CTTATTCTCATAGTGAACATGATGCTGCTGGTGAAGAAGTGAATTGATCTAC	2056	Vollmer J., Jurk M., Lipford GB, Schetter C, Forsbach A, Krieg AM;	PT	Identifying agonists of Toll-like receptor (TLR) signaling activity,	PT	useful therapeutically or prophylactically, comprises contacting an	PT	useful therapeutically or prophylactically, comprises contacting an	PT
Db	1984	CTTGTCTCATAGTGAAGTGTCTGCTGGTGAAGAAGCAGATTACCAAC	2043	XX	XX	XX	XX	XX	XX	XX	XX
QY	2057	TAGAAAAGAAGATATACAGATTGCTCTCATGAGGAATTGRCCTNGCAAGAGCA	2115	PG	Disclosure: SEQ ID NO 84; 342pp; English.	PT	signaling activity.	PT	signaling activity.	PT	signaling activity.

The invention comprises a screening method for identifying agonists of Toll-like receptor (TLR) signalling activity. The method involves contacting an RPMI8256 cell (that expresses a TLR) with a test compound and measuring a test level of TLR signalling activity, where a test level that is positive is indicative of a test compound that is a TLR agonist. The method of the invention is useful for identifying agonists of TLR. The present nucleic acid represents a TLR cDNA sequence.

The invention comprises a screening method for identifying agonists of Toll-like receptor (TLR) signalling activity. The method involves contacting an RPMI 2606 cell (that expresses a TLR) with a test compound, and measuring a test level of TLR signalling activity, where a test level that is positive is indicative of a test compound that is a TLR agonist. The method of the invention is useful for identifying agonists of TLR. The present nucleic acid represents a TLR cDNA sequence.

QY	917	ACAAATTAACTACAATAATGAAAGCATCTGTGAGAAGATTTACTTATCCTAAACGACAT	976
Db	904	ACACTTAACGATAACTGTGAGAAGATCTGACAGGGAGAATTACTTACTCTCGAGAGCAC	963
QY	977	TGAAGACATGACAATAAGAACATATCAGCAGGAAAGTTTCGTGTTTCAGAGAGCTT	1036
Db	964	TGAGTACTGTGATGAGACGACGTCAAACAAACGAGTGTCTCTTCAGAGGCC	1023
QY	1037	TGTACACCGTTTGTGAGTGACATTGATTTAACATTCAAGTACACCTTTA	1095
Db	1024	TATCTCGGTTTGCTGAGATGAACTACAGATCTCTATCTCAGACCCCTTCA	1083
QY	1097	TACACAGCTGTCATCAGCACCAGCACATTGTTACCGACTTACCCAGAAC	1156
Db	1084	TCCACATGGTGGCCCATCCCCAGCTTCACTTCAGTCTCTATCTCAGACCCCTTCA	1143
QY	1157	TTTCACTAGAGTAGTATTGAAAATGTTACCGTAGTTAACTTACCGTACTATCT	1216
Db	1144	TTTTACTGACAGTGTGTTCAAGGCTGTCACCTTAAGAGATGACACATATCT	1203
QY	1217	TACAAAAAATGATTAAAGACCTTCAAGTAGGTCTCATGAGGAGATTCCTT	1276
Db	1204	TACAAGGAAGGTTGAGACTTTTAAGTAGCTCTCTGACTTAAGATATGCT	1263
QY	1277	CCTTGGAATACTGGTGTGACTGAACTTGGATCTGGTAGACATAAGAAACT	1336
Db	1264	CCTCTGGAACTTGGTGTGTTGAGTTCATTCTGACTCTCATGCATGACAGGACAT	1323
QY	1337	GCACCTGGTTGAGAGTATAGTGGTTAATTGTTCTCAATAGCTTACTGACTCTG	1396
Db	1324	GCGCTGGCTGAGACATATGGTTGATGCTTACGCAATAATAAGA	1456
QY	1397	TTTCAGATGTTACCTCCCAGGATCAAGGACTCTTACGCACTCACACACAGGATATGA	1443
Db	1384	TCTTCAGATGTTACCTCCAGGTCAGGTTCTGACCTCTGACCTCACACACAGGATATGA	1623
QY	1457	GGCTTCTAAACAAGCTGAAACTGGAACTTGGAACTGAAACTCTGAAACT	1516
Db	1444	GCATCCCTAAAGATGTCACCCACCTCAGGTTGAGGACTCTGACATCCACT	1503
QY	1517	CTTAACTGACCTCTGGATGTGGAGCTTAGGCTCTGTTGATCATGTC	1576
Db	1504	CCTTAAGTGCACCTCTGGGTGTGGGCCTTOAGCHGCCTTCTGHTGCTGTCACTGACC	1563
QY	1577	ACAACTAGTTCCACCCATGGCTGATTCCTCAGAGCTGCGCAAGAGATGGCAA	1636
Db	1564	AATRACTGAGTTCCATCCCTGAGGATTCTCAGAGCTGTCAGAAATTAGTCC	1623
QY	1637	TTAAACAGGGGACATTCATCCATGTACCTGTGAGCTAGAGATTGTCATAATA	1696
Db	1624	TAAACCGGGAAACACCCATTCATGCAATGCACTGAGCTGAGGACTCTGAGACA	1683
QY	1697	TRAGACCAAGTATCAAGTGAAGAAGTGGTGTAGGGCTGGCTGATCTTAAAGTGTGACTACC	1756
Db	1684	TAGCTGGTAGCAAAAGAACCTTCACTGAGCTGAGGACTCTCAGAGTGTGACTACC	1743
QY	1757	CAGAACTTATGAGGAAAGGCCACTAAAGAACCTTCACTGATCTGATTATCTGGAAACA	1816
Db	1744	CAGAAACTCTTAAAGGAACTGCACTAGGGACTTCACAGTCTCCACTCTGAGATA	1803
QY	1817	TAACTCTGCTCATCGTACCACTGGTGCCACCATCTGGTTGGCTGACTGACCT	1876
Db	1804	CTGTTCTGCTGACTGTACCACTGGGCCACTATGCTGGTACTGGGCTT	1863
QY	1877	CCCTCTGCACTACTGATCTGCCCTGGATCTGGATGTCGCACTGGACCCAGA	1936
Db	1864	TCTCTGCTCATCTGACTGTACCACTGGGCCACTATGCTGGTACTGGGCTT	1923
QY	1937	CTGGGGCGAGGCCAGAACATACCCCTAGAGAAACTCCAAAGAAACCTCTCACTGTTCTGAT	1996
Db	1924	CCAGGAGAGGGCAGACACCTCCCTTAGAGGAACCTCCAGAGAAACCTCCAGTCATG	1983

QY	1997	CCTTTATTCATACTGAACTGATCTGGCTGGTGAAGAATGATGATTGACCTTAC	2056	PT RPMI8226 cell that expresses a TLR with a test compound and measuring TLR signaling activity.
Db	1984	CTTTGCTCTCATCACAGTGAGATGATGATCTGCCTGGGTGAAACGAACTACCCAC	2043	PT XX Disclosure; SEQ ID NO 85; 342pp; English.
QY	2057	TAGAAAGAAGATACTAGATTGTCCTCATGAGAGAACCTGGCCCTGCAAGAGCA	2116	PS XX The invention comprises a screening method for identifying agonists of Toll-like receptor (TLR) signalling activity. The method involves contacting an RPMI8226 cell (that expresses a TLR) with a test compound, and measuring a test level of TLR signalling activity where a test level that is positive is indicative of a test compound that is a TLR agonist. The method of the invention is useful for identifying agonists of TLR.
Db	2044	TAGAGAAAGAGACATCGGGTTGCCCTCATGAGAGAACCTGGCCCTGCAAGAGCA	2103	CC CC The present nucleic acid represents a TLR cDNA sequence.
QY	2117	TGTGGAAATATCATCACTCATTGAGAAGTTACAAGTGAGCTTGTGTC	2176	CC CC The present nucleic acid represents a TLR cDNA sequence.
Db	2104	TGTGGAAACATCATCAATTCTCATGAGAGAACCTGGCCCTGCAAGAGCA	2163	CC CC The present nucleic acid represents a TLR cDNA sequence.
QY	2177	CCAACTTGTCAGACTGACTGTCGCAATTGAACTCTTGGCCATCACATCT	2236	XX Sequence 2421 BP; 640 A; 586 C; 521 G; 674 T; 0 U; 0 Other;
Db	2164	CCACATCCTCATCAGTAGCTGAGCTTGTGTC	2223	Query Match 55.6%; Score 1531.2; DB 13; Length 2421; Best Local Similarity 77.6%; Pred. No. 0; Matches 1848; Conservative 0; Mismatches 533; Indels 0; Gaps 0;
QY	2237	TCTATGAGAGACTTAATACTAATCCTCATCTACTGGAACCATTCCAGAACAGCA	2296	QY 63 CATCATGACCAAGAACAGAACAGACTATGTTAAAGCTTCAATTGTCCTPATGAT 122 Db 30 CAACATCAGCCAAAGAACACCCATCTGGGGATTTCACATTGTTGCCCTGGC 89
Db	2224	TCCCCAGTAGATACACAGAACGTCATGGCACACGGACTTACTGGAATGAGAACAGCA	2283	QY 123 CATAATGTTGAACTGAGAACCTTCTGGCTTAATAGA 2416 Db 90 CTTAAATGTTGTCGQAAGCATGACCCGTTCTTAATGACTGTTGAGCTATTC 149
QY	2297	TTCACACAACTTACACAGTGAAAGCTCTCATGAGCAGGACTTATTGCACTGGC	2356	QY 183 AAAAGGGCTTATCTATGTCCTCAAAGAACCTACCGCTGAACACAGCTTAAAGTAT 242 Db 150 AAACGGAACTTACTCATGTCCTCCAAAGCTGCGACAGAACAAAGCCCTGAGT 209
Db	2344	CTACTGAGAAAGGCAACACTGTCGGCTTTCGGCAACCTAGATTTATGAA	2403	QY 243 GTCTCAGAACTACATCGCTGAGCTCAGGTCCTGACATGAGCTTCTACAGAGTTGAC 302 Db 210 GTCTCAGAACTCTATCTGAGCTGCTGGATCCCTGATATCAGCTTCTGTCAGAGCTGAG 269
QY	2417	ATTAACACTGTCATGAAACAACTGATGATGAACTTAAAAAATTAGAAATTCAA	2476	QY 303 AGTTTGGAGACTTCCCATAACAGATCCAGCTACTTGTGTTAAGTGTGACTTCAA 362 Db 270 AGTTCTGAGACTCTCCACACAGGATACGGCCCTGATTCCATGTTCTGTC 329
Db	2404	AGTTAGCTCTGTCATG---AGGATGATGAACTTGTAA ---CTGGTTCTAA	2456	Db 363 CCAGGATTAGATTTGGATTATCTATAATGAGTTGGAAMAGATACTGCCTAC 422 Db 330 TCAGGACTTGAATCTSGATCTCTACACATGTTGCAAAACATCTCTGTC 389
QY	2477	CTTAAAGAAACCAATTATTTACTGGATGATGTTGAACTGCTGAAAGCTGTC	2536	QY 423 TATGGTGGTTTCAAGGATTAGATCTCTCATCATGATTCAAGGCCATCTG 482 Db 390 TATGGCAGCTGAGGCACTGAGACCTCTCATGATGCTCTGAGCTTGTG 449
Db	2457	CTTAAATAAAC---TGTCAACCTGGCTCTCATGAAACACTGTTGCTTACCTG	2513	QY 483 TAAGGATTGGCACTTATCACACTGAACTGTTCTGGEATTGACTGCTATGAAGCTGCA 542 Db 450 TAAGGATTGGCACTGCTGCACTGAGCTTCTGGGTTAAGTCGCAAGTTCCG 509
QY	2537	GAGGCTCTCATT 2552		Db 543 AAATTAGTTGCTCCAACTGTCATGATGATGATATCTCTGGATTAG 602 Db 510 ACAACTGCACTGCTCCACCTGTCATGCTCACTGATCTGCACTTCTG 569
Db	2514	GAGGTACTTGTGTT 2529		Db 603 AAATTATATAAAAGAAATGAGACAGAACAGAACTGTCATGATGATGATGATG 662 Db 570 GAGTTACATATAAAGGGGGAAACAGAAAGTCTTCAACACCGTCT 629
RESULT 13				
ID	ADU23193	standard; cDNA; 2421 BP.		QY 664 TAAATTATGAGGTTTCAAGGTTCTGAGCTTCTGAGCTTCTGGGTTCAAC 722 Db 630 CCATTGTCCTTCATCAATAGCTGTTCTGTTCTGAGCATGCTGTC 689
AC	ADU23193;			QY 723 TTAGGGTGTCTACACTGACTAATATAATGAGATGAGACTGCACTTCT 782 Db 690 TTAGGACATCTACAGTGTGAACTGATGATGATGAGACTGCACTTCTG 749
XX				QY 783 TAATTATCAGAACTCCAGAGGTCACCTCTGAAATTCTGAACTAACCT 842 Db 750 GACATTCTTACAGAACTCAGAGGTCACCTTATGAACTGACCTCCAGCA 809
DE	27-JAN-2005	(first entry)		QY 843 AGAAACGACTTGGCAATCTGCTCCACCTGTCATGCTCACTGATCTG 902
DE	Murine Toll-like receptor 6 (TLR6)	CDNA sequence - SEQ ID 85.		
KW	screening; Toll-like receptor agonist; TLR agonist; gene; ss; TLR6.			
OS	Mus sp.			
XX	WO2004094671-A2.			
PN	22-APR-2003; 2003US-0464586P.			
XX	22-APR-2003; 2003US-0464588P.			
XX	Vollmer J, Jurk M, Lipford GB, Schetter C, Forsbach A, Krieg AM; WPI: 2004-795573/78.			
PT	Identifying agonists of Toll-like receptor (TLR) signaling activity, useful therapeutically or prophylactically, comprises contacting an			

Db 810 AGAACAACTTGGAAAGTCGGTTAACTTTCCAAATTGCCCCACCGGTGA 869
 Qy 903 ATATCTCAATTACAAATTACAATAATTACAATAATTACAATAATTACAATA 962
 Db 870 GTACCTCAATTACAAATTACAATAATTACAATAATTACAATAATTACAATA 929
 Qy 963 TTCTAAACGCCATTCGAACCATTCGAATAGAACATTCGAATTCGAAGAATTTACTA 1022
 Db 930 CTGGAGACAGACACTGAAGTACTGATGATGAGACAGTCAAACCAAGTGTCCT 989
 Qy 1023 TTACAGACAGACCTTGACACCGTTTCAAGATGAACTTATGATGTTAACATC 1082
 Db 990 TTCAAGAGGGGGCTATACGGGTTGGGTTGGGAGAATCAAGATGCCTCATCTC 1049
 Qy 1083 AGATACACCTTTTACACATGCTGTCCTCATGACCAGCACATTCAAGTTTGAA 1142
 Db 1050 AGACACCCCTTCATCCACATGGTGGCCACCCATCCCAGCTCAATTACATTCTGAA 1109
 Qy 1143 CTTTACCCAGAACGTTTACAGATGATTTGAAAGTTCACGTTAGTAAATT 1202
 Db 1110 CTTTACCCAGAGATGTTTACTGACAGTGTTCAGGCTTCACCTTAAGGATT 1169
 Qy 1203 GGAGACACTTACACAAAAATGATGATAAAGACCTTCAAAAGTAGTCATGAC 1262
 Db 1170 GCAGACACTTACACAAAGAAATGGTTGAGAGTATGGCTTAAAGTACGTTCTCATGAC 1229
 Qy 1263 GAGAGGATATGCTTCTTGGAAATACTGGATTTACTGGATTCTGGATCTGGTAG 1322
 Db 1230 TAAAGATATGCTCTCTGGAACTTGGATTTGAGTTAGTTGAACTCTCATGC 1289
 Qy 1323 ACATAAAGAAACTGCACTGGTGGAGAGTATGGTTAAATTGGCTTAAAT 1382
 Db 1290 ATAGACAGGGCATGGCTGGCTGAGAGATATGGTTGAATTTGCTTCAAT 1349
 Qy 1383 CCTTACTGACTCTGTTCAAGATGTTACCTCCAGGATCAAGTACTGTCACAG 1442
 Db 1350 GCTTACAGGGCTGTGTTCAAGATGCTTACCTCCAAAGGTCAAGGTCTTCACAA 1409
 Qy 1443 CAATAAAATAAGAGGGTCTTAACAAAGTGTAAACTGGAAAGCTTGGAAAGACTAA 1502
 Db 1410 CAACAGGATAATGAGATCCCTAAAGATGTCACCCACCTGAGCTTGGAGAATCAA 1469
 Qy 1503 TGTCTCTTCAATTCTTAAGTGACCTTCTGGAGCTTGGACCTTGT 1562
 Db 1470 TGTAGCATCCACTCTTAAGCTGACCTCTGGTGGGGCTTCAGACCTCTGT 1529
 Qy 1563 ATTGATCATGATCACAAATTCAAGTGTCCACCCATGGCTGATTCTCCAGGAGTGC 1622
 Db 1530 GCTGGTCATCCACCATACTGTTCCATCCCTTGAGGATTCTCCAGGCTGTCA 1589
 Qy 1623 GAAAGATGAGGTCAATAAGAGGGGACATTCATGTTACCTGTGAGCTAAGA 1682
 Db 1590 GAAATATGATTCCTAACAGGGAAACAAACCATTCACATGCACTGTGAGGGA 1649
 Qy 1683 ATTGTCAAATAATGACCAAGTACAGTCAAGTGAAGTGTACAGGCTTGCTGTT 1742
 Db 1650 CTTGTCAGAACATAGGTGTGGTAGGAGAAGTGTGGGGCTGGCTGACTCTA 1709
 Qy 1743 TAAGTGACTACCCAGAAAGTTAGAGGAGGCCACTAAAGGCTTCACATGCTGA 1802
 Db 1710 CAGGTGTGACTACCCAGAAAGCTGAGGACTGACTGGACTGAGGACTTCCACATGTC 1769
 Qy 1803 ATTATCTGCAACATAACTCTGTCGTAACCATGGGACCATGCTGGTTGG 1862
 Db 1770 ACTGTCCTGTCATGACTCTGTCGTCGTCGTCACATGGGCACTATGCGGTGTC 1829
 Qy 1863 TGTGACTGTGACTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1829
 Db 1830 TGTGACTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1889
 Qy 1923 CGAGTGACCAAGACTGGGCCAGGGCAGGACACATACCCCTAGAGAAACTCCAAAGAAA 1982
 Db 1890 TCAGTGGACACAGACAGGGCACAGGGCACATCCCTTAGAGGAACCTCCAGAGAAA 1949

RESULT 14
 ADC78820
 ID ADC78820 standard; DNA; 2381 BP.

XX
 AC
 XX
 DT 01-JAN-2004 (first entry)

DB Human PRO protein coding sequence #25.
 KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; gene; db.

OS Homo sapiens.

XX
 PN WO2003034984-A2.
 XX
 DD 01-MAY-2003.

XX
 PP 15-OCT-2002; 2002WO-US033070.

XX
 PR 19-OCT-2001; 2001US-0340083P.

XX
 PA (GETH) GENENTECH INC.

XX
 PI Goddard A, Gurney AL;

XX
 WPI: 2003-481990/45.

DR P-PSDE; ADC78821.

XX
 PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
 disorder e.g., ulcerative colitis or Crohn's disease.

XX
 PT Medicament for diagnosing or treating cancer or inflammatory bowel

disorder e.g., ulcerative colitis or Crohn's disease.

XX
 Claim 1; SEQ ID NO 49; 327pp; English.

XX
 The invention comprises the amino acid and coding sequences of human PRO
 proteins. The DNA and protein sequences of the invention are useful for
 the diagnosis and treatment of cancer and inflammatory bowel disease

(e.g. ulcerative colitis or Crohn's disease). The present DNA sequence encodes a human PRO protein of the invention.

CC
CC
XX
SQ Sequence 2381 BP; 725 A; 493 C; 450 G; 713 T; 0 U; 0 Other;

Query Match 52.5%; Score 1445; DB 10; length 2381;
Best Local Similarity 76.3%; Pred. No. 0; Mismatches 550; Indels 6; Gaps 1;

Qy	84	ACCTATGTTAAAGCTTCATTGTTGCCATATGCAATAGTGTGACCGAT	143	Db	971	CPTGAACATCTTTCGATAGACACATCAAAATTACAGTCAGTCAGCATGGT	1030
Qy	11	ATCCATRACTASCATCTCCATTGCATTACTTCATGTTAATCCTCAGAT	70	Db	1098	ACACATCTGTCCTCTCATGACCACACATCAAGCTTGGACTTACCCGACGT	1157
Qy	144	CCAGTCCTCCGACGGAATGAAATTGCACTGAGACAAGTCAAAAGAGGTCTATTCTG	203	Db	1158	TTCACAGATAGTATTGAAATCTCCACGTTGAAATTGGAGACCTTCTT	1217
Qy	71	ACATATTCTGAGAAGTGAATTGAAATTGATGATGAGTCAGATCAGAT	130	Db	1091	CTAACAGACACGGTTTGAAATTGGCACCTACTGAGTGGAGACATT	1150
Qy	204	TCCAAAGACATACCGCTGACATGAGCTTCTCAGTGTGAGTTGAGACCTCCATAA	263	Db	1218	ACAAAMAAATGGATTAAAGACCTTCAAGTAGGTCTCATGAGGAGATATGCC	1277
Qy	131	TCTCTAAAGACATCTCCGACAAACACATCTTAATATGAAATTATATGAA	263	Db	1151	ACAAATGAACTCAATAAGAGACTTCAAATAGCTGAATGACTCACAGATG	1210
Qy	264	GCTCAGGCTCTGACATGAGCTTCTCAGTGTGAGTTGAGACCTTCAAACTGAGGT	323	Db	1278	TTCGAAATACTGAGTTAGTGTGAAATTGTTCAATGTTCAATGACTGAGT	1337
Qy	191	GCCTTGACTCTGACATCTACGTGAACTGAGGT	250	Db	1211	TCTGCACAACTTGGATATTAGCCGAAATCTGAATGAGAAAGAGAGTC	1270
Qy	324	CAGATCAGACTTGTGTTAGTTAGTGTGTTCAAGTCACCGGATTAGATTTGGA	383	Db	1338	CACTGGTGTGAGTTAGTGTGAAATTGTTCAATGTTCAATGACTGACTG	1397
Db	251	TGAATCCAGTATCTGATATCAGTGTGTTCAATTGACCAAGGATTGGAATACTGGA	310	Db	1271	TTCTTGACTAAAGTTATTAATGTTAATGTTCAATATACCTACTGACAT	1330
Qy	384	TATATCTCATATACTGTCAAAGAATTCCTCGCCATCTATGTTGAGTTGAGTTGAGETT	443	Db	1398	TTTCAGATGTTACCTCCAGGATCAGGACTGTGTTCAAGGATAATAALGAG	1457
Db	311	TTCGTCGACAAAGTGTGAAATTCTTCACCCCTACTGTGACTCAGACTT	370	Db	1331	TTTCAGTGTGTTACTCCAGATCAGGACTGTGTTCAAGGATAATAALGAG	1390
Qy	444	AGATCTCTCATCACTGATTCAAGCTGTCAGGCTGCCCCTGCAACTTAC	503	Db	1458	CCTTCCTAAACAGTCCTAAACTGGAGCTTGCAGAACTCAATTTGCTTCAT	1517
Db	371	GCACCTGTCATTTAACTGATGTTCAAGTGTGTTCAATGAGCTTTCAGGATT	430	Db	1391	CATTCCAAACAGTCCTAAACTGGAGCTTGCAGAACTTCAGTGTGCTTCAT	1450
Qy	504	ACAACTGAAATTCTGGGATGAGTGTGCTATGAGCTCAAATATTAGATTGTCGCAAT	563	Db	1578	CAATCGTTTCCACCATCGCTGTTCTCAGAGCTGCTCCAGAGATGAGTCAT	1637
Db	431	TCAACTAAATTTCTGGGTGACACACACTGAAATTCTAGTGTGCTGCGAT	490	Db	1511	CAATTGTTTCCACCATCGCTGTTCTCAGAGCTGCTCCAGAGATGAGTCAT	1570
Qy	564	TCTCTCATCTGATCTAAGTTATCCTCTSGATTTAGAAATTATTAATAAGAAA	623	Db	1638	AAAGCGGGGAACTTCATTCATGTTGAGTGTGAGTAAGAGAAATTGTC	1697
Db	491	TCTCTCATCTGATCTAAGTTATCCTCTSGATTTAGAAATTATTAATAAGAAA	623	Db	1571	AARRGGGGGAACTTCATTCATGTTGAGTGTGAGTAAGAGAAATTGTC	1630
Qy	624	TCAGACGAAAGTCTACAAATCTGAAATGCAAAACCTTACCTGTTTTCACCAAC	683	Db	1698	AGACCAAGTACAGTGTGAGTTAGGGGTGCTTACAGTGTGAGTGTGAC	1757
Db	551	AGACCCCTGAGGSGCTTCAGTGTGTTCAAGTTTACCTGTTTACCTGTTTAC	610	Db	1631	AGACCAAGTACAGTGTGAGTTAGGGGTGCTTACAGTGTGAGTGTGAC	1690
Qy	684	TAGTTTATTGCTATCAAAGTAAACATACGTTAATCTTGTGCTTACAGTGTGAC	743	Db	1758	AGAAAGTTAGGAGGAGCCACTAAGGACTTCACAGTCGTTGAAATTATCTG	1817
Db	611	CAAGAAATTCTCATTTTTGGATGTTGCTACTGAACTGTTAGCAATCTGAAAT	670	Db	1691	GGAACGTTATAGAGGAACTACTAAGGACTTCACAGTCGTTGAAATTATCTG	1750
Qy	744	TAATATAAAT-----TGATGATGATCAACTGTCAGTTCAATTAATTATTAGA	797	Db	1818	AACTCTGCTGATGTCACCTGGTGTGAGTTGAGGCTGCTTACAGTGTGAC	1877
Db	671	TAATATCAATGTCGCTAGAGATAACAATGTTCTACTTCCTAGTATCTGGGAA	730	Db	1751	AACTCTGCTGATGTCACCTGGTGTGAGTTGAGGCTGCTTACAGTGTGAC	1810
Qy	798	ACTCACCAGAGAATCTGAACTTACTGAAATTACCTCTGACATGTTACAGTGTGAA	857	Db	1878	CCTCTGCTACTGCTGATGTCACCTGGTGTGAGTTGAGGCTGCTTACAGTGTGAC	1937
Db	731	ACTCTCAACAAATATGAAACGATTCCTGAACTGAAAGTTTCTTAAACGACATT	790	Db	1811	CCTCTGCTACTGCTGATGTCACCTGGTGTGAGTTGAGGCTGCTTACAGTGTGAC	1870
Qy	858	ATGCCCTGGTCAGTCCTCAATTCTGCTGCTGCTGAAACCTGCTCAAGAAACCTCCAGTTCTG	917	Db	1938	TGGGGGAGGGCAGGACATACCTTCAAGAAACCTCCAGTTCTG	1997
Db	791	TCTCTCATCTGATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	850	Db	1871	CGGGCGGGGGGGAGGACATACCTCCAGTTCTGCAAGACATTCAGTTCTG	1930
Qy	918	CAATTAAACAAATATGAAACGATTCCTGAACTGAAAGTTTCTTAAACGACATT	977	Db	1998	TTTATTCTATAGTGTGACATGTTGCTGGTGAAGTGTGTTACCT	2057
Db	851	AAACGCTGAGCTACAGGTCTGCTGACTTCAGAGTTTCTGCTGCTGCTGCTG	910	Db	1931	ATTATTCTATAGTGTGAGGATGTTGAGGATGTTGCAACACT	1990
Qy	978	GAAGACGATGAACTATGAACTATCATGTCACGTTCTGCTGCTGCTGCTGCTG	1037	Db	2058	AGAAAGAAAGTATGAGGACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2117
Db	911	GGAGGCTGTTGTTACACCGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	970	Db	1991	AGAGAGAGTATGAGGACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2050
Qy	2118	TGTGAAATATCATCACTGCAATTGAGAAGAGTTAACAGTCATCTTCCTTCTC	2177				

QY	2178	CAACTTGTCCAGGTTGAGTGGTCGCCATTACGAACTCTATTCGCCATCACATCTT	2237	Query Match 52.5%; Score 1444.2; DB 10; Length 2358;
QY	2111	CAACTTGTCCAGGTTGAGTGGTCGCCATTACGAACTCTATTCGCCATCACATCTT	2237	Best Local Similarity 76.4%; Pred. No. 0; Mismatches 548; Indels 6; Gaps 1; Matches 1789; Conservative 0; Mismatches 548; Indels 6; Gaps 1;
QY	2238	TCTAGGAGGTTATAACTTAATCTCCTACAGGAACTTCCAGAAGAGAT	2297	Qy 88 ATGTTAAAGCTCCATTGTGGCTTAGATCATATAATGTTGAAACCGAATCG 147
Db	2171	TCTAGGAGGTTATAACTTAATCTCCTACAGGAACTTCCAGAAGAGAT	2290	1 ATGATCTGACATTCCTCCATTTCCTACATCTCTGTTAATCTCTGAAATCAA 60
Db	2298	TCCCAACAGTACCAAGCTGAAGGCTCTCATGAGGCTGAGCTTATGGTGGCC	2357	148 TCTCCGAGGAAATGATTSCAGTAGACAGTCAAAGGGCTATTCATGTC 207
QY	2291	CAAGGAAAGAGCAACGTTGGCTTITGGCTAACATTAAGGGCCATTATTA	2350	61 TAATCTGAGAAGTGAAATTAGTGTAGTGTAAAGTCAAAGGTCATCCACGTC 120
Db	2418	ATTACA 2424	2351	Qy 208 AAAGACCTTACCGTGAAGAACACCAGCTAACGTTGGCTTATGAA 2417
QY	2351	GCTGACA 2357	2351	61 AAAGACCTTACCCAGAAACACACATCTAAATAATGCAAAATTATAGCTGAC 180
Db	RESULT 15			Qy 268 CAGSTCTGAGATGAGCTTCTATCAGTAACTGAGTACAGTACGTTGAC 327
Db	ID ADB25536 standard; DNA; 2358 BP.			Qy 381 TGCACTATCTGAGTAAAGATATCCGCCCTCTATGTCAGGTTAGAT 447
XX	ADB25536;			Db 301 TCCCACACAAAGTGGTGGAGATTCTGCCCCCTACTGTGAC 360
XX	29-JAN-2004 (first entry)			Qy 448 CTCTCATTCAGTTCAAGGCCTGCCATCTGTTAGGAAATTGCAACTTACAA 507
DT	Human TLR1 related DNA SEQ ID NO 2.			Db 361 CTGTCATTAATGTCAGTGGTGGATATGTCACCAAGGATTGGATACTGGATT 300
XX	Human; TLR1; cancer; cytostatic; ds; gene.			Qy 508 CTGATTCTGGATTAGTGTGTTAGGAAATTTGAGCTGCAAATTTGAGA 567
XX	Homo sapiens.			Db 421 CTAAATTCTGGTGGTGGACACACTTGTGAAATTCTAGTGTGCTGCAATGTG 420
OS				Qy 568 CACTGCTCTAGTTATCTCTGGATTAGAAATTATATAAAAGAAATG 627
FH	Key Location/Qualifiers			Db 481 CATTGAAATTCAGCAAGGTCTGGCTCTAGGAGACTTATGGGAAAGAGAC 540
CD	1. .2358			Qy 628 ACAGAAGCTAACATTCTGATGCAAACAAACCTTCACCTGTTTACCCA 687
FT	/*tag= a			Db 541 CTGAGGCCCTCTAGACTTACACTGAGACTCTGCACTTGTGTCACAA 600
FT	/product= "TLR1"			Qy 688 TATTCGCTTACCAAGTAACTGAACTTACGTTAGGGCTACAGTACTA 747
FT	/partial=			Db 601 GAATTCATTATTTCGGTGTCACTGAGCTGTGAAATCTGAAATCTPAA 660
FT	/note= "the CDS lacks a stop codon."			Qy 748 ATTAAAT----TGAATGATGACAACGTTCAAGTTCAATTATTCAGAACTC 801
XX	31-JUL-2003.			Db 661 ATCAAATGTTGCTAGAAGATAACAAATGTTCTACTCTAATGATCTGGGAACCT 720
PD	26-DEC-2002; 2002W0-JP013642.			PA (TAKE) TAKEDA CHEM IND LTD.
XX	27-DEC-2001; 2001JP-00398165.			QY 802 ACCAGAGGTTAACCTACTGTGTTACCCATGAAACAGCTGGAAATGC 861
PA	(TAKE) TAKEDA CHEM IND LTD.			Db 721 CAAACAAATCCAAAGTTCACTCTACCTAACACATGAAACACTGGAAATGC 860
XX	Hikichi Y, Katsuyama R, Kakoi Y, Nishizawa S;			QY 862 CTGGTCAGGTCTTCAAATTCTTGGCCAACCTGGAAATCTGAAATTCAC 921
DR	WPI: 2003-598709/56.			Db 781 TCTTGTGATCTCCAGTGTGTTGGCATACACTGTGTGTTCTCAATCAAC 840
XX	P-PSSB; ADE25535.			QY 922 TAACAATTAATGAAAGCATCTGGAAAGAGTTACTTCTAAACGICATGAA 981
PT	Treatment and prevention for cancer of the e.g. digestive system, liver and lung.			Db 841 GTGAGGCTACGGTCAGCTGACTTCTAGAGATTGTGTTCTGGCACTTGTGAG 900
XX	Disclosure; Page 80-84; 98pp; Japanese.			QY 982 GCTATGACATAGACATTCACCAACCAAGTTCTGGCAACCTGGAAATCTGAA 1041
CC	The invention relates to the treatment and prevention of cancer comprising a compound that inhibits the activity of protein or peptide fragment of a fully defined amino acid sequence TLR1 given as SEQ ID NO 1. TLR1 is useful in the treatment and prevention of cancers of the large intestine, mammary glands, lung, prostate, digestive tract, stomach and liver. TLR1 gene expression is detected in breast cancer tissue. The present sequence is that of a human TLR1 encoding DNA sequence.			Db 901 GCCTTGCTATACACCAAGTTGTCAGCATGTTCTGGCAAGTATCTGAT 960
CC				QY 1042 ACCGGTTCTGGATGACATATTGATGTTACCATTTGAGTACACCTTTATAC 1101
CC				Db 961 GAATCTTCTGGATGACATCAAAATTCTGAGTCTGTCAGCAAGCTGGCCAC 1020

QY 1102 ATGCTGTGTCATGCCAACAGCACATTCAAGTAACTTACCCAGAACGTTTC 1161
Db 1021 ATCTTGGCCATCCAAATTACCCCTCTCCTCATTTGGAATTTCACATTCCTTA 1080
QY 1162 ACAGATGTTATGAAAGTTCACCGTTAGTTAATGGAGACACTTATCTTCAA 1221
Db 1081 ACAGACACGGTTTGAAATGTCGGCACCTTACTAGTGGAGACATTATTTCAA 1140
QY 1222 AAAATGGATAAGACCTTCAAGTAGGTTCTGAGAGGATATGCCTCTTGT 1281
Db 1141 ATGAACTGATAAAGACTTCAAATACTGAGATAGCATACAGATGAGTCCTG 1200
QY 1282 GAAATACGTGATGTTAGCTGGAACTTGGAATCTGGTAGACAGACTTACAA 1341
Db 1201 CAAACAATGGATTAGGCCAGATTCTGTAAGTATGAAAGAGAGGAGCTG 1260
QY 1342 TGGTTCAGAGATACTGGTTAAATGTCCTCAATAGCTTACTGACCTGTT 1401
Db 1261 TGGACTAAAGTTATTAAGTTAAATGTCCTCAATACTACTGACATTTTC 1320
QY 1402 AGATGTTACCTCCAGGATCAAGGACTTCTTCACAGCATATAAGGGTT 1461
Db 1321 AGATGTTACCTCCAGGATCAAGGACTTCTTCACAGCATATAAGGGTT 1380
QY 1462 CCTAAACAAAGTGTAAACTGAAAGCTTGGCAGAACTCAATGTTCTTCATTTA 1521
Db 1381 CCTAAACAAAGTGTAAACTGAAAGCTTGGCAGAACTCAATGTTCTTCATTTA 1440
QY 1522 ACTGACCTTCCAGGATCAAGGACTTCTTCACAGCTCCAGAGTAACTTCAACAT 1581
Db 1441 ACTGACCTTCCAGGATCAAGGACTTCTTCACAGCTCCAGAGTAACTTCAACAT 1500
QY 1582 TCAAGTTCACCCATGGCAGTTCTCCAGAGCTGCCAGAGTGGCTTATGATGATCAAT 1641
Db 1501 TCAGTTTCCCAGGATCAAGGACTTCTTCACAGCTCCAGAGTGGCTTATGATGATCAAT 1560
QY 1642 CGAGGGACAAATCCATCCAATGACCTGAGCTAGAGAATTGTCAAATAATAGAC 1701
Db 1561 CGAGGGACAAATCCATCCAATGACCTGAGCTAGAGAATTGTCAAATAATAGAC 1620
QY 1702 CAAGTATCAAGTGAAGTGTAGGGCTGGCTGATCTTAACTGTGACTTACCCAGAA 1761
Db 1621 CAAGTATCAAGTGAAGTGTAGGGCTGGCTGATCTTAACTGTGACTTACCCAGAA 1680
QY 1762 AGTTATAGAGGAGCCACTTAAAGGACTTCACTGCTGAAATTCTGGACATACT 1821
Db 1681 AGTTATAGAGGAGCCACTTAAAGGACTTCACTGCTGAAATTCTGGACATACT 1740
QY 1822 CTGCTGATCGTACCATGGGCCACCATGCGGTGGTGGACTGTCACCTCCCTC 1881
Db 1741 CTGCTGATCGTACCATGGGCCACCATGCGGTGGTGGACTGTCACCTCCCTC 1800
QY 1882 TGCATCTACTTGGATCTGGTACCTGGCCCTGGTACCTGGTGGACTGTCACCTCCCTC 1860
Db 1801 TGCATCTACTTGGATCTGGCCCTGGTACCTGGTGGACTGTCACCTCCCTC 1941
QY 1942 CGCAGGGCAGGACATACCTTAGAGAAGTCCAAAGAACCTCCAGTTCTGTT 2001
Db 1861 CGCAGGGCAGGACATACCTTAGAGAAGTCCAAAGAACCTCCAGTTCTGTT 1920
QY 2002 ATTCACTATAGTGAACATGATCTGCTGGTAAAGTGAATGTCACCTTACCTAGAA 2061
Db 1921 ATTCACTATAGTGGCACGATCTCTGCTGAGAATGTCACCTTACCTAGAA 1980
QY 2062 AAAGAAGATATACAGATTGCTCTGAGAGGAACTTCTGCTGAGAATGTCACCT 2121
Db 1981 AAAGAAGATATACAGATTGCTCTGAGAGGAACTTCTGCTGAGAATGTCACCT 2040
QY 2122 GAAATATCATCAACTGATGAGAGTACAAGTCACCTTCTGCTGAGAATGTCACCT 2181
Db 2041 GAAATATCATCACTGATGAGAGTACAAGTCACCTTCTGCTGAGAATGTCACCT 2100

QY 2182 TTGTCGAGAGTGTGCGATAGAACCTATTTGCCATCACAACTCTTCAT 2241
Db 2101 TTGTCGAGAGTGTGCGATAGAACCTATCTGCGATCACAACTCTTCAT 2160
QY 2242 GAGGAGCTAACTTAATCTTAACTCTTCACTTACTGGAAACCCATTCCAGAAACGATTC 2301
Db 2161 GAGGAGCTAACTGCTTAACTCTTCACTTACTGGAAACCCATTCCAGAAACGATTC 2220
QY 2302 AACAACTTACAGTGAAGGCTCTATGAGCAGGGACTTATTCACAGGCCAG 2361
Db 2221 ACCGTTATCACAAAGTCTCAAACTGCTATGGCTAACAGGACTTATGGATGCCAG 2280
QY 2362 GAGAAGGCAACGTCGGCTTTCGGCTAACATAGAGCCGCTTTATGAAATA 2421
Db 2281 GAAAGGCAACGTCGGCTTTCGGCTAACATAGAGCCGCTTTATGAAATA 2340
QY 2422 ACA 2424
Db 2341 ACA 2343

Search completed: June 4, 2006, 23:39:59
Job time : 1689 secs

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Page 1

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2006, 23:18:43 ; Search time 15573 Seconds
(without alignments)
11304.646 Million cell updates/sec

Title:	US-10-732-796A-11
Perfect score:	2753
Sequence:	1 agatattggactcatatcaa. ttcccaaatggatctgtg 2753
Scoring table:	IDENTITY_NUC Gap=10.0 , Gapext 1.0
Searched:	6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters:	12732272
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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7: gb_st:*
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13: gb_in:*
14: gb_on:*
15: gb_ba:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2753	100.0	2753	CQ903893 Sequence
2	2749.8	99.8	2758	CQ726557 Sequence
3	2749.8	99.9	2758	AR659471 Sequence
4	2749.8	99.9	6758	AR659631 Sequence
5	2749.8	99.9	6758	AR659757 Sequence
6	2749.8	99.9	173834	AC108044 Sequence
7	2748.8	99.8	2760	AC087047 Sequence
8	2748.8	99.8	2760	CQ903892 Sequence
9	2748.8	99.8	2760	AR659345 Sequence
10	2748.8	99.8	2760	AK339047 Sequence
11	2748.8	99.8	2760	AB020807 Sequence
12	2748.2	99.8	78986	AC115626 Homo sapi
13	2748.2	99.8	182019	AC054388 Homo sapi
14	2747.2	99.8	2760	E33464 Novel Toll-
15	2727.8	99.1	2940	AX576262 Sequence
16	1925.2	69.9	177804	AB210286 Sus scrofa
17	1907.2	69.3	194826	AC163791 Bos tauru
18	1860.2	67.6	2559	AB208698 Sus scrofa

ALIGNMENTS

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE			
RESULT 1	CQ903893	CQ903893 Sequence	CQ903893	Sequence	2753 bp	DNA	1 linear	PAT 16-NOV-2004
LOCUS	CQ903893	Sequence	CQ903893	from patent	2753 bp	DNA	1 linear	PAT 16-NOV-2004
DEFINITION	CQ903893	79	CQ903893.1	GI: 55785292
ACCESSION	CQ903893	79	CQ903893.1	GI: 55785292
VERSION	CQ903893.1	GI: 55785292
KEYWORDS
SOURCE	Homo sapiens	(human)	Homo sapiens	(human)	Homo sapiens	(human)	Homo sapiens	(human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.							
REFERENCE	1	Vollmer,J., Jurk,M., Lipford,G.B., Schetter,C., Forsbach,A. and Krieg,A.M.						
AUTHORS		Methods and products for identification and assessment of tlr ligands						
TITLE		Patent: WO 2004094671-A 79 04-NOV-2004; Coley Pharmaceutical GmbH (DE); Coley Pharmaceutical Group, Inc. (US)						
JOURNAL								
FEATURES		Location/Qualifiers						
		1. -2753 /organism="Homo sapiens" /mol:type="unassigned DNA" /db_xref="taxon:9606"						
ORIGIN								

Query Match Best Local Similarity 100.0%; Score 2753; DB 2; Length 2753; Matches 2753; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

Qy 1 AGAATTGGACTCATTCAGTGTGCTGAGAGACACCCCTTAGGTAGGCCACTGC 60

Db 1 AGAATTGGACTCATTCAGTGTGCTGAGAGACACCCCTTAGGTAGGCCACTGC 60

Qy 61 AACATCATGACCAGAACAGAACATTATGTTAAAGCTTCATTTGTTGCGCTTATG 120

Db 61 AACATCATGACCAGAACAGAACATTATGTTAAAGCTTCATTTGTTGCGCTTATG 120

Qy 121 ATCATATAAGTGGAAACAGAGATCCTGGACGGAATTAATTGAGTAGAGACAG 180

Db	121 ATCATAATAGTTGGACCAGATCCAGTCTCGAGGAATTGGAGACAG 180	Qy	1261 ACGAAGGATAATGCCCTTGAAATACGGATGTTGGAAATTCTTGGAATCTGT 1320
Qy	181 TCAAAGAGGCTTATTCTGTCAGTCTGAAAGACCTAACGCTGAAACAGTCTAGAT 240	Db	1261 ACAGAGGATAATGCCCTTGAAATACGGATGTTGGAAATTCTTGGAATCTGT 1320
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Qy	241 ATGTCAGACTACATCGCTGAGCTTCAGTGGCTCATGAGCTTCAGTGGCT 300	Db	1321 AGACATAAGAAACTGCACTTGGTTGAGAGTAGTGGTTAAATTGTCITCAAT 1380
Db	241 ATGTCAGACTACATCGCTGAGCTTCAGTGGCTCATGAGCTTCAGTGGCT 300	Qy	1381 ATGCTPACTACTCTGTTAGTGGTTACCTCCAGATCAAGGTTACTGAGCTTCAGTGC 1440
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Db	301 ACAGTTTGAGACTTCCATAACAGATCAGACTTGTTAGTGGTTCAAGTC 360	Qy	1441 AGCAATAATAAGAGCGTCTAACAGTCTAACAGTCTAACAGTCTAACAGTCTAACAGTGC 1500
Qy	361 ACCAGGATTAGAATATTGAGTTATCTAACTCAGTGCAGAAGATATCCGCCAT 420	Db	1441 AGCAATAATAAGAGCGTCTAACAGTCTAACAGTCTAACAGTCTAACAGTCTAACAGTGC 1500
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Qy	421 CCTATGTCAGTTCAGGCATTAGATCTCTCATCAATGATTGGCTGGCCATC 480	Db	1501 AATGTTGCTTCATACTTAACTGACCTCTCTGGATGTTGGCACTTACGCTTCT 1560
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Db	481 TGTAAAGGAAATTGGCAACTTACACACTGATTCTGGATTGAGTGTAGCTG 540	Qy	1621 CAGAAGTGGTCAATAAGCAGGGACATCCATCAGTACTCTGAGCTAGA 1680
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Qy	601 AGAAATTATTTATAAAGAAATGAGACAGAACTACAAATTGAACTTGAAAC 660	Db	1681 GAATTGTCAAAATATAGACCAACTATCAGTGAAGTGTAGGGCTGGCTGATCT 1740
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Db	721 ACTTCTAGGTTCTTACACTACTAATTAACTGATGAGACTCTGCAAGTTTC 780	Qy	1861 GCTGTCAGTGTGACCTCCCTCTGATCCTACTTGGATCTGGCTGGTACGATGTC 1920
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Qy	841 ATAGAAACGACTGGAAATGCCGTGAGCTCTTCAATTCTTGCCCCAACCTGT 900	Db	1921 TGCCAGTGGACCCAGACTCGCGCGAGGCCAGGAACATACCTTGTAGAGACTCAAAGA 1980
Db	841 ATAGAAACGACTGGAAATGCCGTGAGCTCTTCAATTCTTGCCCCAACCTGT 900	Qy	1981 AACCTCCAGTTCATGCTTATTCTCATATAGTGAACATGATCTGCTCTGGTGAAGT 2040
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Db	961 TATTCTAAAGACATGAGCATTGACAGACATACAGAACCTAACGAGCTTCTG 1020	Qy	2101 GTCCCTGGCAGAGCATGTCAGAATATCATCAACTGCATGAGAGACTTACAGTCC 2160
Qy	1021 TTTCAAGAGACTTACAGAGCTTACAGTAGTATTGAAATGTCACCTGTTAACTT 1080	Db	2101 GTCCCTGGCAGAGCATGTCAGAATATCATCAACTGCATGAGAGACTTACAGTCC 2160
Db	1021 TTTCAAGAGACTTACAGAGCTTACAGTAGTATTGAAATGTCACCTGTTAACTT 1080	Qy	2161 ATCTTCTTGTCTCCAACTTGTGCACTGCTGTTCTGAGTGTGGCTCATCACTT 2220
Qy	1081 TCGATACACCTTATACACATGCTGCTCATGCAACAGACATTCAGTTTG 1140	Db	2161 ATCTTCTTGTCTCCAACTTGTGCACTGCTGTTCTGAGTGTGGCTCATCACTT 2220
Db	1081 TCGATACACCTTATACACATGCTGCTCATGCAACAGACATTCAGTTTG 1140	Qy	2221 GCCATACAACTCTCTCATGAGAGTCTAACTTCTCATCTTACTGAAACC 2280
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Qy	1201 TTGGAGACACTTACACAAAAATGGATAAAGACCTTCAAGTGGCTCATG 1260	Db	2281 ATTCCACAGAACAGCATCCACACAGTACCAAGCTGAGGCTCTCATGAGCGCG 2340
Db	1201 TTGGAGACACTTACACAAAAATGGATAAAGACCTTCAAGTGGCTCATG 1260		

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Db 2641 AGCCAGTCCTCTCGTTTATCATTATGTTCAATTCATGCCCTACAA 2580
QY 2701 ATGCTCAGTTTCAGCTCCCTCCACTCTCTTCCAAATGGATTCTGTG 2753
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RESULT 2

CQ726557 Q0726557 2758 bp DNA linear PAT 03-FEB-2004
LOCUS Sequence 12491 from Patent WO20068579.
DEFINITION C0726557
ACCESSION CQ726557.1 GI:42289938
VERSION 1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Humanxons, such as nucleic acid arrays, comprising a majority of
thereof transcripts, for detecting expression and other uses
Patent: WO 02068579-A 12491 06-SEP-2002;
PE Corporation (US)
FEATURES Source
1. . 2758 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 99.9%; Score 2749; DB 2; Length 2758;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2751; Conservative 0;

QY 1 AGAAATTGGACTCATCAAGATGCTCTGAGAAGACAACCTTTAGGACTGC 60
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Db	1442	AGCAATAAAGAAAGGGTCTTAACAGTGTTAACTGGAGCTTGCAAGACT	1501	QY
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Db	1502	AATGTTGCTTCACTCTTTAACGTTCTCTGGATCTGGAGCTTAGACCTTCT	1561	QY
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Db	1562	GATTGATCATGATCAGAACATTCTAGTTCCACCACTGGGATCTTCCAGGCGC	1621	QY
QY	1621	CAGAGATGAGGTCATAAAGCAGGGACATTCATCAATGTTACCTGTGAGCTG	1680	Db
Db	1622	CAGAGATGAGGTCATAAAGCAGGGACATTCATCAATGTTACCTGTGAGCTG	1681	QY
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Db	1682	GAATTGTCAAATAATAGACCAAGTCAAGTGAAGTGTAGGG3TGGCTGTATCT	1741	QY
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Db	1742	TATAAGTGTGACTACCCGAAACTTATGAGGAGGCCACTAAAGGACTTCACTGCT	1801	QY
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Db	1802	GAATTATCTGCACAACTCTGGTACGTGACATGGGACCACTGGGTGTTG 1861	QY	
QY	1861	GCTGTTGACTGTGACCTCCCTCTGCATCTACTGGTACGTGACATGGGACCACTGGGTGTTG 1920	Db	
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Db	1922	TECCAGTGACCCAGACTGGGCCAGGCCAGAACATACCCCTAGAGAACTCCAAAGA	1981	QY
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Db	1982	AACCTCCAGTTGATGCTTATTCTAGTGACATGATCTGCTGGGTGAAGT	2041	QY
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Db	2042	GAATTGTTACCTTACCTAGAAAGAGATATACGATTTGTCCTCATGAGGAACTT	2101	QY
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Db	2102	GRCCCTGCAAGGAGATGTGGAAATATCATCACGATGAGGAGTACAGTCC	2161	QY
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Db	2162	ATCTTGTGTTGCTCCAACTTGTCCAGAGTGAGTGTGGCTCATAGACTCTT	2221	QY
QY	2221	GGCCATACAATCTCTCATGAGGATCTAATACCTAATCTCTCATGAGGACCC	2280	Db
Db	2222	GGCCATACAATCTCTCATGAGGATCTAATACCTAATCTCTCATGAGGACCC	2281	QY
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QY	2341	ACTTATGCACTGGCCAAAGGAGAAACGAACTGGGCTCTTGGCTAACATGAG	2400	Db
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Db	302	ACAGTTTGAACTTCCATACAGATCAGACTTGTGATTAGTGTTCAGTC	361	Db	1382	ATGCTTACTGACTCTTTCAGATGTTACTCCAGGATCAAGTACTGTATTCAC	1441
Qy	361	AACAGGATTAGAATTGGATTATCTCAATACTAGTCCAAAGATRCCGCGAT	420	Qy	1441	AGCAATAATAAAGAGGCTTCTAACAGTCGTAAGTGGAGCTTGCAGAACTC	1500
Db	362	ACCAGGATTAGAATTGGATTATCTCAATACTAGTCCAAAGATRCCGCGAT	421	Db	1442	AGCAATAATAAAGAGGCTTCTAACAGTCGTAAGTGGAGCTTGCAGAACTC	1501
Qy	421	CTCATGTTGAGTTTCAGGCATTTAGATCTCATTCATGATTCAAGGCCATG	480	Qy	1501	AATGTTGCTTCATCTTAACTGACTCTCTGGATGTCGACGTTAGCAGCTTCT	1560
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Db	482	TGTAAAGGAACTTGGCACTTATCACACTGATTCTGGGATTTAGTGAAGCTG	541	Db	1562	GTATTGATCATGATCACAACTTCACTGTTCTGGGATTTAGTGAAGCTG	1621
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Db	602	AGAAATTATTAATATAAGAAATGAGACAGAAAGTCACTGATGCAAAACC	661	Db	1622	CAGAATGAGGTCATTAAGCAGGGACAACTTCAGTCAATGCAAACC	1681
Qy	661	CTTCACTTGTGTTTACCCACTAGTTATCGTATCCAGTACATACAGTTAAT	720	Qy	1681	GAATTGTCALAAATATGAGCAAGTATCAAGTCACTGAGTTAGGGCTGCTCATCT	1740
Db	662	CTTCACTTGTGTTTACCCACTAGTTATCGTATCCAGTACATACAGTTAAT	721	Qy	1682	GAATTGTCALAAATATGAGCAAGTATCAAGTCACTGAGTTAGGGCTGCTCATCT	1741
Qy	721	ACTTGGGCTTACAACACTAATATTAATTTAGATGTCGACACTGCAAGTTC	780	Qy	1741	TATAAGTGTGACTACCCAGAAAGTTATAGGAGAACCCACTAAAGGACTTACAGTCT	1800
Db	782	ATTAATTTATCAGACTACCACTACAGAGGTTCAACTTACCTTACCCAC	841	Db	1742	TATAAGTGTGACTACCCAGAAAGTTATAGGAGAACCCACTAAAGGACTTACAGTCT	1801
Qy	841	ATAGAACGACTGTTGAAATGCTGTCAGACTTCTTCATTTGGCCAAACTGTG	900	Qy	1801	GAATTATCCTGCAACATAACTCTGTGTCACCATCGTGCACACATGCTGTTG	1860
Db	842	ATAGAACGACTGTTGAAATGCTGTCAGACTTCTTCATTTGGCCAAACTGTG	901	Db	1862	GAATTATCCTGCAACATAACTCTGTGTCACATCTGATGTCACCATCGTGCACATGCTGTTG	1861
Qy	901	GAATATCTCAATTACAATTACAATAATGAAAGCATCTGTCAGAGGTTACT	960	Qy	1921	TGCCAGTGGACCCAGACTCGCGCGAGGCCAGGAACATACCCATTAGAGAACTCCAAAGA	1980
Db	902	GAATATCTCAATTACAATTACAATAATGAAAGCATCTGTCAGAGGTTACT	961	Db	1922	TGCCAGTGGACCCAGACTCGCGCGAGGCCAGGAACATACCCATTAGAGAACTCCAAAGA	1981
Qy	961	TATTCTAAAGCACATGAAAGCATGACAAATAGACATACAGGAGTTCTG	1020	Qy	1981	AACCTCCAGTTCTGCTTTTATTCATATAGTGAACATGATTCTGCTCGGGTAAAGT	2040
Db	962	TATTCTAAAGCACATGAAAGCATGACATAGACATACAGGAGTTCTG	1021	Db	1982	AACCTCCAGTTCTGCTTTTATTCATATAGTGAACATGATTCTGCTCGGGTAAAGT	2041
Qy	1021	TTCACAGACAGCTTGTGACACCGTTCTGAGATGACATTAGTAACTCATT	1080	Qy	2041	GAATGGTACTTACCTGAAAGAGATAACAGATGTTCTCATGAGGAACTT	2100
Db	1022	TTCACAGACAGCTTGTGACACCGTTCTGAGATGACATTAGTAACTCATT	1081	Db	2042	GAATGGTACTTACCTGAAAGAGATAACAGATGTTCTCATGAGGAACTT	2101
Qy	1081	TCAGATACACCTTTACAGATGCTGTCATGCACCAAGCACATTCAAGTTG	1140	Qy	2101	GTCCCTGCAAGAGCATGTCGAAATATCATCAACTGATGAGGAACTTACAGTCC	2160
Db	1082	TCAGATACACCTTTACAGATGCTGTCATGCACCAAGCACATTCAAGTTG	1141	Db	2102	GCCCCGCGAGAGATGTCGAAATATCATCACTGATGAGGAACTTACAGTCC	2161
Qy	1141	ACTTTACCCGAGACCTTACAGATGTTGAAAGATGTCACCTTAGTAA	1200	Qy	2161	ATCTTGTGTCCTCCAACTTCTGCTGAGTGGTGGCCACATCAACACTPATTT	2220
Db	1142	ACTTTACCCGAGACCTTACAGATGTTGAAAGATGTCACCTTAGTAA	1201	Db	2162	ATCTTGTGTCCTCCAACTTCTGCTGAGTGGTGGCCACATCAACACTPATTT	2221
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QY	2581 AACATGTTCATCGGGAACTGAGCTAGGCTAGGGGTGAGGTAGCTGCAAGTAGAAC	2640	Db
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QY	2701 ATGCTAGTTTCAGCTCTCACTCTGTTCCAATGATGCTGTG 2753	2754	Db
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RESULT 4			ORIGIN
LOCUS	AR659631	6758 bp	DNA
DEFINITION	Sequence 672 from patent US 6900016.	linear	PAT 13-JUN-2005
VERSION	AR659631.1	GI:67595671	
KEYWORDS	Unknown.		
SOURCE	Unclassified.		
ORGANISM			
REFERENCE	1 (bases 1 to 6758)		
AUTHORS	Venter, J.C., Zhang, J.N., Liu, X., Rose, W., Cravchik, A., Kalush, F., Naik, A., Subramanian, G. and Woodage, T.		
TITLE	Polymorphisms in known genes associated with inflammatory autoimmune disease, methods of detection and uses thereof		
JOURNAL	Patent: US 6900016-A 672 31-MAY-2005;		
FEATURES	Location/Qualifier		
source	1. . 6758 /organism="unknown" /mol_type="genomic DNA"		
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Query Match	99.9%; Score 2749.8; DB 2; Length 6758;		
Best Local Similarity	99.9%; Pred. No. 0;		
Matches	2751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
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QY	181 TCAAAAGGGCTATTCAAGTCCAAAGACCTACCGTGAACCAAGCTAGT 240	3022	Db
Db	2182 TCAAAAGGGCTATTCAAGTCCAAAGACCTACCGTGAACCAAGCTAGT 2241	1080	QY
QY	241 ATGCTCAGACTACATCGCTGACGTTCTGACATGAGCTTCTATCAGAGTC 300	3081	Db
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QY	301 ACAGTTGAGACTTCCATAAGAACCTACCGTACTGATTAAGCTTCAAGTC 360	3142	Db
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Db 3502 AATGGTGCTTCATTCTTAAGTGCCTTCGATGTGGCACTTTAGCAGCTTCTGGAC 3561
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 Db 3742 TATAAGTGTGACTACCCAGAAGTATAGAGGAGCCACTAACAGGTTACAGTCT 3801
 Qy 1801 GATTTCTGCAACATAACTCTGCTGATGTCACCATGCG3GCCACCATGCGTTG 1860
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RESULTS 5 AR659757
 AR659757 LOCUS Sequence 6758 bp DNA linear PAT 13-JUN-2005
 AR659757 DEFINITION Sequence from patent US 6900016.
 AR659757 ACCESSION AR659757
 AR659757 VERSION AR659757.1 GI:67595817
 AR659757 KEYWORDS SOURCE
 Unknown.
 Unclassified.
 1 (bases 1 to 6758)
 Venter, J.C., Zhang, J.N., Liu, X., Rowe, W., Cravchik, A., Kalush, F.,
 Naik, A., Subramanian, G. and Wooldridge, T.
 TITLE Polymorphisms in known genes associated with inflammatory
 autoimmune disease, methods of detection and uses thereof
 JOURNAL US 6900016-A 798 31-MAY-2005;
 Applera Corporation; Norwalk, CT
 FEATURES Location/Qualifiers
 source 1..6758
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 ORIGIN
 Query Match 99.9%; Score 2749.8; DB 2; Length 6758;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2751; Conservative 99.9%; Pred. No. 0;
 Mismatches 0; Indels 0; Gaps 0;
 Db 2002 AGATTTGGACTCATATCAAGATGCTTGAAGAGAACACCTTGTAGGATAGCCACTGC 2061
 Qy 61 AACATCTGGACAAAGAACCTATTGTTAAAGCTCCATTGTTGCCATTG 120
 Db 2062 AACATCTGGACAAAGAACCTATTGTTAAAGCTCCATTGTTGCCATTG 2121
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 Db 2362 AACAGGAGTTAGAATTTGATTCTCATGCTGAAAGATACTCGCCAT 2421
 Qy 421 CCTATGTTGAGCTTCCATACAGATCAGCTACTGTTGATTAAGTGTGTTCAAGTC 480
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QY	541	CAAAATTAGATTGCTGCCATGTCACTGCATCAAGTAACTCCCTTGAGTTA	600	QY	1621	CAGAAGATAGGTCAATAAAGCAGGGGACAATCACTCCAAGTACACTGTGAGTA	1680
Db	2542	CAAAATTAGATTGCTGCCATGTCACTGCATCAAGTAACTCCCTTGAGTTA	2601	Db	3622	CAGAAGATAGGTCAATAAAGCAGGGGACAATCACTCCAAGTACACTGTGAGTA	3681
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Db	2602	AGAAATTATTAATAAGAAATGAGACACAAAGTCACTGCATCAAGTAACTCC	2661	Db	3682	GAATTGTCAAAATATAGACCAAGTATCACTGAAGTGTAGGGCTGGCTGAT	3741
QY	661	CTTCACCTGTTTACCCACTACTTATCGPATCCAGTCACTGAATGCAAACC	720	QY	1741	TAAAGTGTACTACCCAGAAAGTTAGAGGAAGCCACTAAGGACATTCACT	1800
Db	2662	CTTCACCTGTTTACCCACTACTTATCGPATCCAGTCACTGAATGCAAACC	2721	Db	3742	TATAGTGTACTACCCAGAAAGTTAGAGGAAGCCACTAAGGACATTCACT	3801
QY	721	ACTTAGGCTCTACACTAATTAATTGATGAGCACTGCAAGTTC	780	QY	1801	GAATTATCTGCAACATAACTCTGCTGATCGTCACTTCCACATCTGCTG	1860
Db	2722	ACTTAGGCTCTACACTAATTAATTGATGAGCACTGCAAGTTC	2781	Db	3802	GAATTATCTGCAACATAACTCTGCTGATCGTCACTTCCACATCTGCTG	3861
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QY	841	ATAGAACAGCTGGAATSCCTGTCAGACTCTTCAATTCTTGCCAAACTGTG	900	QY	1921	TGCCAGTGGACCCAGACTCGCGCAGGGCAGAACATACCTTGTAGAGA	1980
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QY	901	GAATATCTCAATTACAAATTAACTTAATTGAAAGCATCGTGAGAGATT	960	QY	1981	AACCTCCAGTTCTGCTTATTCTATAGTGAACATGATTGCTGGTCAA	2040
Db	2902	GAATATCTCAATTACAAATTAACTTAATTGAAAGCATCGTGAGAGATT	2961	Db	3982	AACCTCCAGTTCTGCTTATTCTATAGTGAACATGATTGCTGGTCAA	4041
QY	961	TATTCTAAAGACATGAAAGCATCGTGACAAATAGAACATATCACGAA	1020	QY	2041	GAATTGTTACTCTACTGAAAGAACATAGATTTGCTCTGATGAGAACT	2100
Db	2962	TATTCTAAAGACATGAAAGCATCGTGACAAATAGAACATATCACGAA	3021	Db	4042	GAATTGTTACTCTACTGAAAGAACATAGATTTGCTCTGATGAGAACT	4101
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QY	1081	TCAGATACACCTTATACAGCTGTCTCATCACCAAGACATGTTG	1140	QY	2161	ATCTTTGTTGTCMCCCACTTGCCAGTAGTGGTGGCCATTCAAGCT	2220
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QY	1141	ACTTACCCAGAACGCTGTTAACAGTAGTTTGTGAAAMAGTTCAC	1200	QY	2221	GCCCCATCACATCTCTCTGATGAGATCTAACTACTATCCICATCTACT	2280
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QY	1201	TGAGAACACTATCTTACAAAAAATGGATAAAGACCTTCAAGTGGTCATG	1260	QY	2281	ATCCACAGACAGCATCCACACAGTACACAGCTGAGCTGAGTACAG	2340
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QY	1261	ACGAAGATAGCTCTTGTGAATACTGCTGAGCTGAAATCTGTT	1320	QY	2341	ACTTATGTCAGTGCCTGAGGAGAAAGAACCTGTTGGCTCTTGGGTAA	2400
Db	3262	ACGAAGATAGCTCTTGTGAATACTGCTGAGCTGAGCTTGTGATCTG	3321	Db	4342	ACTTATGTCAGTGCCTGAGGAGAAAGAACCTGTTGGCTCTTGGGTAA	4401
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Db	3322	AGACATAAAGAAACTGCACTGGGTGAGGATGATGTTGGTTAATTC	3381	Db	4402	GCGCCTTTATATGAAATTACACTGACTGACTGAAACATGATGTTGAA	4461
QY	1381	ATGCTTACTGACTGTTAACGAGAACGACTATGATGTTGGTTAATTC	1440	QY	2461	AAATTGAAATTCACTTAACTGAAACATGATGTTGAAATCTTAA	2520
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QY	1441	AGCATAAATAAGAGCGCTCTAACACAGTGAACCTGCAAGACTC	1500	QY	2521	CGTAAGTAACTGCTGGAGGCTCCATTACCTGATGTTGAAAGACTA	2580
Db	3442	AGCATAAATAAGAGCGCTCTAACACAGTGAACCTGCAAGACTC	3501	Db	4522	CGTAAGTAACTGCTGGAGGCTCCATTACCTGATGTTGAAAGACTA	4581
QY	1501	ATGCTTACTGACTGTTAACGAGAACGACTATGATGTTGGTTAATTC	1560	QY	2581	AAACATGTTCACTGCTGGAGGCTCCATTACCTGATGTTGAAAGACTA	2640
Db	3502	ATGCTTACTGACTGTTAACGAGAACGACTATGATGTTGGTTAATTC	3561	Db	4582	AAACATGTTCACTGCTGGAGGCTCCATTACCTGATGTTGAAAGACTA	4641
QY	1561	GTATTGATCATGATCACATTGAGCTTCCACCCATGGTGTCTTCAGAC	1620	QY	2641	AGCCAGTCCTCTGGTTAACATGAAAGCTCTTGTGAGTACAG	2700
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QY	2701	ATGCTTACTGACTGCTGGAGGCTCCATTACCTGATGTTGAAAGACTA	2753	QY	2701	ATGCTTACTGACTGCTGGAGGCTCCATTACCTGATGTTGAAAGACTA	2753

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ORIGIN

Query Match 99.9%; Score 2748; DB 2; Length 2760;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2750; Conservative 0; MisMatches 3; Indels 0; Gaps 0;

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 Db 301 ACAGTTTGAACTTCCATACAGATCCAGCTTCAAGTTCAGGTG 360
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 QY 541 CAAAATTAGATTGCTGCCAATGTCACACTGCTCAAGTATATCCCTCTGGTTA 600
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 Db 1922 TGCCAGTGGACCAAGCTGGCGAGGGCAGGACATACCCCTGAGAGACTCAAAGA 1981
 QY 1981 AACCTCCAGTTTCACTGCTTATTCTATAGTGAACATGATCTGCTGGTGAAGAAGT 2040
 Db 1982 AACCTCCAGTTTCACTGCTTATTCTATAGTGAACATGATCTGCTGGTGAAGAAGT 2041

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QY	2161	ATCTTGTGTTCTCAACTTGTGAGGTGAGTGAGGTGAGGTACAGTCC	2161	Best Local Similarity	99.8%; Pred. No. 0;
Db	2162	ATCTTGTGTTCTCAACTTGTGAGGTGAGTGAGGTACAGTCC	220	Matches	2750; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY	2281	ATTCACAGAACAGCATCCAAACAAGTACCAACAACGCTGAGGCTCATGAGG	2340	QY	61 AACATGAGCAAGAACACCTATGTTAAAGCTCCATTGAGCTTCATCTACTG
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QY	2341	ACTTAATGCGGTGSCCAACAGAGAAAGCAGCGGGCTTTCGGCTAACATAGA	2400	QY	181 TCAAAGAGGTATCATGTTCAAAAGACTACCGTGAAGAACAAAGCTTAG
Db	2402	ACTTAATGCGGTGSCCAACAGAGAAAGCAGCGGGCTTTCGGCTAACATAGA	2401	Db	182 TCAAAGAGGTATCATGTTGGCTAACATAGA
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Db	2462	AATTAGAACATCACTTACATGAAACATTATTACTTGTGAGTGTGATAGTACGT	2521	Db	184 ATGCTCGAGACTACATCGCTGAGCTTCAGCTCTGAGCTTCTATCAGAG
QY	2521	CCTAAGTGTCTTATGAAATTACATGACTAGTCTACTGAAACAAATGTAATCTTAA	2580	QY	185 ATGCTCGAGACTACATCGCTGAGCTTCTGAGCTTCTATCAGAG
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ORGANISM	Homo sapiens				
REFERENCE	1. Vollmer,J., Jurk,M., Lipford,G.B., Schetter,C., Forbach,A. and Krieg,A.M.				
AUTHORS					
TITLE	Methods and products for identification and assessment of tlr ligands				
JOURNAL	Patent: WO 200404671-A 78 04-NOV-2004;				
FEATURES	Coley Pharmaceutical GmbH (DE); Coley Pharmaceutical Group, Inc. (US)				
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DEFINITION Sequence 100 from patent US 6900016.
ACCESSION AR65345
VERSION AR65345..1 GI:6759537
KEYWORDS
ORGANISM Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 2760)
AUTHORS Venter,J.C., Zhang,J.N., Liu,X., Rowe,W., Cravchik,A., Kalush,F.,
TITLE Polymorphisms in known genes associated with inflammatory
autoimmune disease, methods of detection and uses thereof
PATENT: US 6900016-A 100 31-MAY-2005;
JOURNAL Applera Corporation; Norwalk, CT
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ACCESSION AB020807

VERSION AB020807.1 GI:5006247

KEYWORDS TLR6

SOURCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE Takeuchi, O., Kawai, T., Sanjo, H., Copeland, N.G., Gilbert, D.J., Jenkins, N.A., Takeda, K. and Akira, S.

TITLE TLR6: A novel member of an expanding toll-like receptor family

JOURNAL	Gene 231 (1-2), 59-65 (1999)	QY
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REFERENCE	2 (bases 1 to 2760)	QY
AUTHORS	Akira,S and Takeuchi,O.	Db
TITLE	Direct Submission	Db
JOURNAL	Submitted (05-DEC-1998) Shizuo Akira, Hyogo College of Medicine, Department of Biochemistry; Mukogawa-cho 1-1, Nishinomiya, Hyogo 663-8501, Japan (E-mail:sakira@bjken.osaka-u.ac.jp, Tel:81-798-45-6357, Fax:81-798-46-3164)	QY
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QY	121	ATCATATACTGACCAAGAACGAAACCTATTGTAAGCTTCATTGTGCTTATG	180	Db	45544	TGGAGCACTTCTTAAAGGACTTCAAGGCTAAAGGACTTCAAGGCTCAG	45485
Db	46624	ATCATATACTGACCAAGAACGAAACCTATTGTAAGCTTCATTGTGCTTATG	46555	QY	1261	ACGAGGATAGCCTTGGAAATCTGGATGTTGCTGAATTCAGTCTGTT	1320
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Db	46504	ATGCTCAGAACATCATGCTGACCTTCAGCTCTGACAGACGTTCTCAGCTG	46445	QY	301	ACAGTTGACACTTCCATACAGATCCAGCTACTGTTAAGTGTTCAAGTTC	360
Db	46384	ACAGGAGTAAAGGACTTCCATACAGATCCAGCTACTGTTAAGTGTTCAAGTTC	46325	QY	46444	ACGTTTGACACTTCCATACAGATCCAGCTACTGTTAAGTGTTCAAGTTC	46385
QY	361	ACAGGAGTAAAGGACTTCCATACAGATCCAGCTACTGTTAAGTGTTCAAGTTC	420	Db	46444	ACGTTTGACACTTCCATACAGATCCAGCTACTGTTAAGTGTTCAAGTTC	46385
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Db	45844	CAATATCTCAATATTACAATTAACATTAATGAAAGCATCTGAAAGAGTTACT	45785	QY	961	TATTCAGACAGCTTGTGACCCGTTCTGAGATGACATATGTTAACATT	1020
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Db	45784	TATTCAGACAGCTTGTGACCCGTTCTGAGATGACATATGTTAACATT	45725	QY	1021	TATTCAGACAGCTTGTGACCCGTTCTGAGATGACATATGTTAACATT	1080
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44404	ACTTTATTCGAGTGGCCAGGAGAAAGCAAATGGGAGCTTGTGAGGCTCATGAGGAGGG	44405	JOURNAL	Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
44464	ATTCCACAGCACGAGTCCAACAGTACAGAACAGCTGAGGCTCATGAGGAGGG	44465	REFERENCE	3 (bases 1 to 162019)
2341	ACTTTATTCGAGTGGCCAGGAGAAAGCAAATGGGAGCTTGTGAGGCTCATGAGGAGGG	2400	AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Bouaslanskiy,L., Boukhaite,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearlano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Gaiagan,J., Gardina,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horizon,L., Holland,J.C., Iliev,I., Johnson,J., Kann,J., Karatas,A., Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lenoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R., Medrini,J., Meneus,L., Minora,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Maylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pianini,C., Polara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testayre,S., Theodore,J., Trell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
2401	GCCGCTTAAATAGGAATTACACTAGTCACTGAAACATGAACTGAGGAAAGCAGGGCGGG	2460	QY	44461 AATTTAGGAATTCACTTAACTAGAACCATTATTACTTGATGATGTTGAGTAGACTG 2520
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SEQUENCE	28 unordered pieces.			
ACCESSION	AC024388			
VERSION	44104			
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SOURCE	Homo sapiens (human)			
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REFERENCE	(bases 1 to 182019)			
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.			
TITLE	Homo sapiens chromosome 4, clone RP11-115L8			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 182019)			
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavskyi,L., Boukhalebt,B., Brown,A., Burkett,G., Campopiano,A., Castie,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearlano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Dearlano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Fenster,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J., Gardner,S., Ginde,S., Goettke,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Jones,C., Kann,J., Karatas,A., Klein,J., Lander,E., Linton,L., Nusbaum,C., O'Neil,D., O'Donnell,P., O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pianini,C., Polara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testayre,S., Theodore,J., Trell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.			
COMMENT	Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA			
On May 12, 2000 this sequence version replaced gi:7229904.	All repeats were identified using RepeatMasker:			
Smit,A.F.A. & Green,P. (1995-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html				
Center: Whitehead Institute/MIT Center for Genome Research				
Center code: WIBR				
Web site: http://www-seq.wi.mit.edu				
Contact: sequence_submission@genome.wi.mit.edu				
Center project name: L6635				
Center clone name: 115_L_8				
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-----	-----	Summary Statistics		
-----	-----	100% of reads		
Chemistry: Dye-terminator	Big Dye	100% of reads		
Assembly program: phrap	version 0.960731			
Consensus quality: 158219 bases at least Q40				
Consensus quality: 16827 bases at least Q30				
Consensus quality: 174699 bases at least Q20				
Insert size: 133000; agarose-fp				
Insert size: 179319; sum-of-contigs				
Quality coverage: 5.2 in Q20 bases; agarose-fp				
Quality coverage: 3.8 in Q20 bases; sum-of-contigs				
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* NOTE: This is a 'working draft' sequence. It currently				
* consists of 28 contigs. The true order of the pieces				
* is not known and their order in this sequence record is				
* arbitrary. Gaps between the contigs are represented as				
* runs of N, but the exact sizes of the gaps are unknown.				
* This record will be updated with the finished sequence				
* as soon as it is available and the accession number will				
* be preserved.				
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1 1331: gap of 100 bp				
1 1332: contig of 1341 bp in length				
2 2672: contig of 100 bp				
2 2772: gap of 100 bp				
2 2773: contig of 1896 bp in length				
2 4668: gap of 100 bp				
2 4669: 4768: gap of 100 bp				
2 4769: 7007: contig of 2239 bp in length				
2 7008: 7107: gap of 100 bp				
2 9577: contig of 2470 bp in length				
2 9578: 9677: contig of 100 bp				
2 9678: 10880: contig of 1203 bp in length				
2 10881: 10980: gap of 100 bp				

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QY	124627 TATAAGTGTGACTACCCAGAGTTATAGGGAGCCACTAAAGGACTTCACTGCT 124686	DEFINITION Novel Toll-like receptor and gene thereof.
QY	1801 GAATTGTCAAATATAGACCAAGTCAAGTCAAGTCAAGTTAGGGCTGGCTGATTC 1860	ACCESSION E34464
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QY		KEYWORD JP 2000126900-2/1.
QY		SOURCE Homo sapiens
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	REFERENCE	Hominidae: Homo.
AUTHORS	1 (bases 1 to 20)	
Shinra, S. and Takeuchi, S.		
TITLE	Novel Toll-like receptor and gene thereof	
JOURNAL	Patent: JP 2000128900-A 1 09-MAY-2000;	
SCIENCE & TECH AGENCY	OS	
COMMENT	Homo sapiens (human)	
PN	JP 2000128900-A/1	
PD	09-MAY-2000	
PP	26-OCT-1998 JP 1998304110	
PR		
PI	SHIZUO SHINRA, SATOSHI TAKEUCHI	
PC	C07K14/715, C12N5/10, C12N5/09, C12R1:91, (C12P21/02, C12R1:91), (C12N5/10, C12N5/00, C12N5/09, C12R1:91)	
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Fri Jun 9 14:07:30 2006

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27955665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_hc:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gss1:
12: gb_gss2:
13: gb_gss3:
14: gb_gss4:
15:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	% Match	Length	DB	ID	Description
1	2387.8	86.7	2391	14	AY416997	AY416997	RESULT 1
2	2198.2	79.8	2391	14	AY416998	AY416998	LOCUS
3	1537.4	55.8	2350	6	AK137502	AK137502	DEFINITION
4	1525.8	55.4	2388	14	AY416999	AY416999	genomic survey sequence.
5	1525.4	55.4	2522	6	AK154253	AK154253	ACCESSION
6	1439.4	52.3	2806	6	AL05062	AL05062	VERSION
7	1267.4	46.0	3051	10	DY109015	DY109015	KEYWORDS
8	1104.9	40.7	3020	6	AK143721	AK143721	SOURCE
9	22.0	1342	10	DY779572	DY779572	TITLE	
10	571.4	20.8	573	9	Da673961	Da673961	JOURNAL
11	562.4	20.4	564	9	DB143901	DB143901	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
12	553	20.1	609	9	Da619469	Da619469	COMMENT
13	529.8	19.2	772	2	BG963497	BG963497	This sequence was made by sequencing genomic exons and ordering them based on alignment/Qualifiers
14	527.2	19.2	698	8	CK980331	CK980331	FEATURES
15	526.6	19.1	684	4	CB554647	CB554647	gene
16	526	19.1	570	9	Da383103	Da383103	/gene="TIR6"
17	522.2	19.0	698	5	CK966621	CK966621	/locus_tag="HCM6077"
18	516	18.7	572	9	Da677587	Da677587	ORIGIN
19	505.4				CD702179	CD702179	
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45							

RESULTS

ALIGNMENTS

C	20	501	18.2	501	8	CR748796	CR748796
C	21	480.2	17.4	525	2	BP92285	BP92285
C	22	480.2	17.3	677	12	CE100991	CE100991
C	23	472	17.1	695	4	BV763747	BV763747
C	24	484.4	16.9	829	9	DN935328	DN935328
C	25	482.6	16.8	630	12	CL00155	CL00155 gbs1 VM5 -
C	26	462.4	16.8	568	9	DB140055	DB140055
C	27	46.8	16.2	616	7	BS079205	BS079205
C	28	434.6	15.8	779	1	AM004250	AM004250
C	29	429.2	15.6	485	7	BS006222	BS006222 RC2-BN012
C	30	423.8	15.4	570	12	CB286667	CB286667 tigr-gss-
C	31	42.2	15.0	564	7	BR080763	BR080763 ut81911.Y
C	32	412.2	15.0	554	7	BR080760	BR080760 231760 MA
C	33	411.6	15.0	742	5	CD368967	CD368967 RCI-23-3
C	34	411	14.9	656	5	CF763276	CF763276 CES00083
C	35	401	14.6	713	11	BH331283	BH331283 CH230-125
C	36	385.8	14.0	501	7	BE448296	BE448296 ut81911.Y
C	37	381.4	13.9	500	10	DY19346	DY19346 000928EM
C	38	379	13.8	583	11	AZ243185	AZ243185 RCI-23-3
C	39	378.6	13.8	858	7	BS911102	BS911102 601662486
C	40	373.4	13.6	689	4	CA438677	CA438677 UT-H-DTRI-
C	41	356	12.9	664	5	CF911104	CF911104 A06100D9-
C	42	352.4	12.8	700	3	BG623316	BG623316 UI-H-FIL
C	43	350.4	12.7	480	7	BR080533	BR080533 231515 MA
C	44	349.8	12.7	667	3	BQ003287	BQ003287 UI-H-E11-
C	45	348.2	12.6	360	5	CF136926	CF136926 UI-HF-BN0

Query Match	Score	DB 14;	Length	2391;
Best Local Similarity	86.7%			
Matches 2389;保守性 99.9%; 预测数 0; 错配数 2; 插入数 0; 缺失数 0;				
Y	67	ATGACCAAGAACGAACTATGTAAAGCTCCATTGTCATGATA	126	
b	1	ATGACCAAGAACGAACTATGTAAAGCTCCATTGTCATGATA	60	
Y	127	ATAGTTGGACCGAATCCAGTTCMCCGAGGAATGAAATTGCAGTAGACAAGTCAAA	186	
b	1	ATAGTTGGACCGAATCCAGTTCMCCGAGGAATGAAATTGCAGTAGACAAGTCAAA	120	
Y	187	AGAGGCTTATTATGTTCAAAGAACCTACCGCTGAAACCAAGTCTAGATGCT	246	
b	121	AGAGGCTTATTATGTTCAAAGAACCTACCGCTGAAACCAAGTCTAGATGCT	180	
Y	247	CAGACTACATCGCTGAGCTCAGGTTCTGACATGAGCTTCAGITGCAAGTT	306	
b	181	CAGACTACATCGCTGAGCTCAGGTTCTGACATGAGCTTCAGITGCAAGTT	240	
Y	307	TTCGAGACTTCCCATAACAGAACTTCAAGGCTTCAAGTTCAGCAG	366	
b	241	TTCGAGACTTCCCATAACAGAACTTCAAGGCTTCAAGTTCAGCAG	300	
Y	367	GATTAGATATTGGATTATCTCATATCAGTCAGTCAGATTCCTCCATCTT	426	
b	301	GATTAGATATTGGATTATCTCATATCAGTCAGTCAGATTCCTCCATCTT	360	
Y	427	GTGAGTTTCAGGCATTAGATCTCTTCAATCATGATTCAGGCTGCCATCTT	486	
b	361	GTGAGTTTCAGGCATTAGATCTCTTCAATCATGATTCAGGCTGCCATCTT	420	
Y	487	GAATTGCGAACTTATCACACTGAACTTCTGCGATGAGTGCTATGAAGTCSAAAA	546	
b	421	GAATTGCGAACTTATCACACTGAACTTCTGCGATGAGTGCTATGAAGTCSAAAA	480	
Y	547	TAGATTCTGCCATTGCTCAGTCAGTCATCACTGATATACCTCTGGATTAGAAT	606	
b	481	TAGATTCTGCCATTGCTCAGTCAGTCATCACTGATATACCTCTGGATTAGAAT	540	
Y	607	TATTATTAAGAAATGAGACAGAAAGTCTACAAATTCTGAATGCAAAACCTCAC	666	
b	541	TATTATTAAGAAATGAGACAGAAAGTCTACAAATTCTGAATGCAAAACCTCAC	600	
Y	667	CTTGTTCACCCACTAGTTATGCGPATCCAGTGACATATCAGTAACTTTA	726	
b	601	CTTGTTCACCCACTAGTTATGCGPATCCAGTGACATATCAGTAACTTTA	660	
Y	727	GGGTGCTTAACTGACTAAATTAAATTGATGAGTACACTGTCAGTTCTAA	786	
b	651	GGGTGCTTAACTGACTAAATTAAATTGATGAGTACACTGTCAGTTCTAA	720	
Y	787	TTTTTACAGAACTCACCAGAGGTCAACCTACTGAAATTACCTCAACCATAAGAA	846	
b	721	TTTTTACAGAACTCACCAGAGGTCAACCTACTGAAATTACCTCAACCATAAGAA	780	
Y	847	ACGACTTGGAAATGCCCTGGTCAGACTTCAATTCTTGGCCAAACCTGGAAT	906	
b	781	ACGACTTGGAAATGCCCTGGTCAGACTTCAATTCTTGGCCAAACCTGGAAT	840	
Y	907	CTGAAATTACAAATTAAACATAATTGAAAGCATTCGTGAGAAAGATTACTTCT	966	
b	841	CTGAAATTACAAATTAAACATAATTGAAAGCATTCGTGAGAAAGATTACTTCT	900	
Y	967	AAACGACATGAAAGCATTCGTGAGACATAGACATACGACCAAGTTCTGTTCA	1026	
b	901	AAACGACATGAAAGCATTCGTGAGACATAGACATACGACCAAGTTCTGTTCA	960	
Y	1027	CAGACAGCTTGTACCCGTTCTGAGATGAAATTGATGTTACCTTGAGAT	1086	
b	951	CAGACAGCTTGTACCCGTTCTGAGATGAAATTGATGTTACCTTGAGAT	1020	
Y	1087	ACACCTTATACACATGCGTGTGTCCTCATGACCAAGCATTCAGTTGTGACATT	1146	

Db	1021	ACACTTITATCACAGCTGCTCCATGCCACAGCATCAAGTTTGACTT	1080
Qy	1147	ACCCAGAAGCTTCAZAGATGATTTGAAATGTCAGGTAGTTAATGGAG	1205
Db	1081	ACCCAGAAGCTTCAZAGATGATTTGAAATGTCAGGTAGTTAATGGAG	1140
Qy	1207	ACACTTCTAACAAAATGCTTAAGCCTTCAAAAGTAGTCACTGAGAG	1255
Db	1141	ACACTTCTAACAAAATGCTTAAGCCTTCAAAAGTAGTCACTGAGAG	1200
Db	1201	GATATGCTCTTGGAAATCTGATGTTAGCTGGAAATCTTGAATCTGGAGAC	1250
Qy	1267	GATATGCTCTTGGAAATCTGATGTTAGCTGGAAATCTTGAATCTGGAGAC	1326
Db	1327	AAAGAAACTGACTTGGGTTAGAGTAGTGTGTTAATTGTCCTCAAATATGCT	1386
Db	1261	AAAGAAACTGACTTGGGTTAGAGTAGTGTGTTAATTGTCCTCAAATATGCT	1320
Qy	1387	ACTGACTCTGTTTCAAGTGTACCTCCAGGATCAGGATATTGATCTTGGAA	1416
Db	1321	ACTGACTCTGTTTCAAGTGTACCTCCAGGATCAGGATATTGATCTTGGAA	1380
Qy	1447	AAATAAGAGGCTTCTAACAGTCTGCTGTTAAACTGGAAAGCTTGCAGAACT	1506
Db	1381	AAATAAGAGGCTTCTAACAGTCTGCTGTTAAACTGGAAAGCTTGCAGAACT	1416
Qy	1507	GCTTCAATTCTTAACTGACCCTCTCGATGCGCAGCTTACAGCTTCTGTT	1566
Db	1441	GCTTCAATTCTTAACTGACCCTCTCGATGCGCAGCTTACAGCTTCTGTT	1500
Qy	1567	ATCATGATCACATTCAGTTGCCACCATCGCTGATCTTCCAGACTGCGA	1626
Db	1501	ATCATGATCACATTCAGTTGCCACCATCGCTGATCTTCCAGACTGCGA	1550
Qy	1627	ATGAGGTCATAAAAGCAGGGGACATCCATGTAACAGTCTGAGGAAATT	1686
Db	1561	ATGAGGTCATAAAAGCAGGGGACATCCATGTAACAGTCTGAGGAAATT	1620
Qy	1687	GTCAAATATGAGCAAGTACAAGTGAGGTTAGAGGCTGCTGATTCTTAAAG	1746
Db	1621	GTCAAATATGAGCAAGTACAAGTGAGGTTAGAGGCTGCTGATTCTTAAAG	1680
Qy	1747	TGTGACTACCCGAGAAGTATAAGGAGCCACTAAAGGACTCTACAGTCGAA	1806
Db	1681	TGTGACTACCCGAGAAGTATAAGGAGCCACTAAAGGACTCTACAGTCGAA	1740
Qy	1807	TCCTGCACATAACTCTGCTGATGTCACCATGCGCACCATGCTGGTGTG	1866
Db	1741	TCCTGCACATAACTCTGCTGATGTCACCATGCGCACCATGCTGGTGTG	1800
Qy	1867	ATGTGACCTCCCTCTGATCTACTTGGATCTGCCCTGTTATCTCAGGATGTTGCCAG	1925
Db	1801	ATGTGACCTCCCTCTGATCTACTTGGATCTGCCCTGTTATCTCAGGATGTTGCCAG	1860
Qy	1927	TGCAACCGAGCTGGCGAGGGCAGGACATACCTCTAGAGAACTCCAAGAACCT	1966
Db	1861	TGCAACCGAGCTGGCGAGGGCAGGACATACCTCTAGAGAACTCCAAGAACCT	1920
Qy	1987	CAGTTCATGCTTATTCTCATATGAGCATGTTCTGCTGGTGAAGAGTATG	2046
Db	1921	CAGTTCATGCTTATTCTCATATGAGCATGTTCTGCTGGTGAAGAGTATG	1980
Qy	2047	GTACCTACTAGAAAGAGATATACATCACTGCTGAGAGACTACAGTCCT	2106
Db	2041	GTACCTACTAGAAAGAGATATACATCACTGCTGAGAGAGTACAGTCCT	2040
Db	1981	GTACCTACTAGAAAGAGATATACATCACTGCTGAGAGAGTACAGTCCT	2226
Qy	2167	GTITGCTCCAACTGTCAGAGTGCTGCTGGCATTACGACTCTATTGCCC	2166

Db 2101 GTTTGTCTCCAACTTGTCCAGAGCTGAGCTGGCATAGAACCTATTTGCCAT 2160 Qy 187 AGAGGTTTACAGTCAGTCCAAAGCCTACCGTGAAACCAACTCTAGATATGCT 246
 Qy 2227 CACAATCTCTTCTCATGAGGACTAATPACTTAATCTCATTTACTTGAAACCATTCA 2286 Db 121 AGAGGTTTATTCAGTGTCCAAAGCCTACCGTGAAACCAACTCTAGATATGCT 180
 Db 2161 CACAATCTCTTCTCATGAGGACTAATPACTTAATCTCATTTACTTGAAACCATTCA 2220 Qy 247 CAGAACATACATGCTGAGCTCAGGCTCTGACATGAGCTTCTATAGAGTGAGCT 306.
 Db 2287 CAGAACAGCAATCCAACTACCAAGCTGAAAGCTCTCATGAGCACGGACTTAT 2346 Db 181 CAGAACATACAGCTGAGCTCAGGCTCTGACATGAGCTTCTATAGAGTGAGCT 240
 Db 2221 CAGAACAGCTTCCAAACAACTGACACATGAGCTGAAAGCTCTCATGAGCACGGACTT 2280 Qy 307 TTGAGACTTCCATAACAGAATCCAGCTACTGTTAAGTGTTCAGTCACCAAG 366
 Qy 2347 TTGAGACTTCCATAACAGAATCCAGCTACTGTTAAGTGTTCAGTCACCAAG 300 Db 241 TTGAGACTTCCATAACAGATCCAGCTACTGTTAAGTGTTCAGTCACCAAG 300
 Db 2281 TTGCAAGGCCAAAGGAAAGCAACGTTGGCTCTTGGCTACATTAGAGCGCT 2406 Qy 367 GATTAGAATTGCTATCTCATTAACGTCACAGTCCAAAGATCTCTGCATCTATT 426
 Qy 2407 TTTAATGAAATTAACTACTGACTGAAACAACTATGTAATCTTA 2457 Db 301 GATTAGAATTGCTATCTCATTAACGTCACAGTCCAAAGATCTCTGCATCTATT 360
 Db 2341 TTAAATGAAATTAACTACTGACTGAAACAACTATGTAATCTTA 2391 Qy 427 GTGAGTTTCAGGCAATTAGTACTCTGATTCATGTTCAAGGCCATCTGTAG 486
 RESULT 2 Db 361 GTGAGTTTCAGGCAATTAGTACTCTGATTCATGTTCAAGGCCATCTGTAG 420
 AY416998 AY416998 2391 bp DNA linear GSS 17-DEC-2003 Qy 487 GAATTGCAACTTATCAACTGAAATTCTCTGGATTGACTGCTATGAGCTGAA 546
 LOCUS DEFINITION Pan troglodytes TLR6 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. Db 421 GAATTGCAACTTATCAACTGAAATTCTCTGGATTGACTGCTATGAGCTGAA 480
 ACCESSION AY416998 VERSION AY416998.1 Qy 547 TTGATTGCTCCAATGCTCACTGCATCTAGTATATCCTCTGGATTAGAA 606
 KEYWORD GSS. Db 481 TTGATTGCTCCAATGCTCACTGCATCTAGTATATCCTCTGGATTAGAA 540
 SOURCE Pan troglodytes (chimpanzee) Qy 607 TTTATAAAAGAAATGAGACAGAGAAGTCTACAAATCTGAATGCAAACCTTCAC 666
 ORGANISM Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan. Db 541 TTTATAAAAGAAATGAGACAGAGAAGTCTACAAATCTGAATGCAAACCTTCAC 600
 REFERENCE 1. (bases 1 to 2391) Qy 667 CTGTGTTTCACTTCAACCTAAGTTATGCTATCCAAAGTACATTCAGTTAATCTTA 726
 AUTHORS Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tarenbaum,D.M., Civello,D.R., Liu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M. Db 601 CTGTGTTTCACTTCAACCTAAGTTATCTCTGGATTAGAA 660
 TITLE Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003) Qy 727 GGGTCTTCAACTGCTAATTAATGATGATGACAATGCTGAGTTCTCA 786
 JOURNAL 14671302 PUBLMED 2 (bases 1 to 2391) Db 661 GGGTCTTCACTTCAACCTAAGTTATCTCTGGATTAGAA 720
 REFERENCE Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tarenbaum,D.M., Civello,D.R., Liu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M. Db 787 TTTTAACTGAGACTCACCAGAGGTTCAACCTTACTGATTACCTCAACCATA 846
 AUTHORS Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA Db 721 TTTTAACTGAGACTCACCAGAGGTTCAACCTTACTGATTACCTCAACCATA 780
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Db 847 AGCAGTTGAAATGCTGGTCAGAGTCTTCATTTGGCCRAACCTGGRATAT 906
 FEATURES JOURNAL 1. Direct Submission Db 781 AGCAGTTGAAATGCTGGTCAGAGTCTTCATTTGGCCRAACCTGGRATAT 840
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 /locus_tag="HCM6077" Db 901 AAACGCAATGAAAGCAATTGAAATGAACTATCAAGAACAGTTCTGTTCA 1026
 ORIGIN Qy 967 AAAACGCAATGAAAGCAATTGAAATGAACTATCAAGAACAGTTCTGTTCA 1026
 Db 901 AAACGCAATGAAAGCAATTGAAATGAACTATCAAGAACAGTTCTGTTCA 960
 Db 1027 CAGACAGCTTGTACACCGTTTCTGAGATGAACTATGATGTTAACCTTCAGAT 1086
 Db 961 CAGACAGCTTGTACACCGTTTCTGAGATGAACTATGATGTTAACCTTCAGAT 1020
 Qy 1087 ACACCTTTACACAGCTGCTCTCATCCACCAAGCACATCAGTTTGACTT 1146
 Best Local Similarity 92.6%; Pred. No. 0; Matches 2215; Conservative 0; Mismatches 176; Indels 0; Gaps 0; Db 1021 ACACCTTTACACAGCTGCTCTCATCCACCAAGCACATCAGTTTGACTT 1080
 Qy 67 ATGACCAAGCAAGCAAGAACCTATGTTAAAGCTTCATTGTTGCTATGCTATA 126 Qy 1147 ACCCAGAGCTTCAAGATGAACTATGTTGAAAGATGTCACGTTAACCTTCAG 1206
 Db 1 ATGACCAAGCAAGCAAGAACCTATGTTAAAGCTTCATTGTTGCTATGCTATA 126 Db 1081 ACCCAGAGCTTCAAGATGAACTATGTTGAAAGATGTCACGTTAACCTTCAG 1140
 Qy 127 ATGTTGAACTGAGCTTCAAGAACCTATGTTAAAGCTTCATTGTTGCTATGCTATA 186 Qy 1207 ACACCTTTACACAGCTGCTCTCATCCACGTTAACCTTCAG 1266
 Db 61 ATAGTGTGAACTGAGCTTCAAGAACCTATGTTAAAGCTTCATTGTTGCTATGCTATA 120 Db 1141 ACACCTTTACACAGCTGCTCTCATCCACGTTAACCTTCAG 1200
 Qy 1267 GATATGCCCTTTGAAACTGGAATTGCTGTTAGCTGAACTTCTTGAGATCTGGTAGACAT 1326

AUTHORS	Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Built, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kamapin, A., Matsuda, H., Batyalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chotila, C., Corbani, I.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.R., Maglott, D.R., Maiwald, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavani, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C., Setou, M., Shihada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanebe, Y., Wells, C., Wilming, L.G., Wynsleath-Boris, A., Yanagisawa, M., Yang, J., Yang, L., Yuan, Z., Zavolian, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Satoh, K., Shiraki, T., Waki, K., Kawai, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itou, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shimagawa, A., Yoshida, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E., and Hayashizaki, Y.
CONSRM	FANTOM Consortium
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420 (6915), 563-573 (2002)
PUBMED	12466851
REFERENCE	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Zavolian, M., Davis, M.J., Wilming, L.G., Aldinis, V., Allen, J.E., Ambesi-Impiombato, A., Asweiler, R., Aturali, R.N., Bailey, T.L., Bansal, M., Baxter, J., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Daley, E., Dalrymple, P., de Boni, C., Delila, Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Furuki, S., Gariboldi, M., Gutticich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Humblet, L., Iacono, M., Ieko, K., Iwana, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoch, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kiana, H., Koilias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kuurockhin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, M., Liu, J., Lujan, S., McWilliam, S., Madan, B., Madara, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakuchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishimura, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavani, W.J., Pavesi, G., Peoole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S., Sandelin, A., Schneider, C., Schonbach, C., Sekine, K., Semple, C.A., Seno, S., Sesha, L., Shang, Y., Shibusawa, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Spelvin, S., Stupka, E., Sugiyama, K., Sultan, R., Takehara, T., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Teicher, J., Techmann, S.A., Ueda, H.R., van Nieuwegen, E., Verardo, R., Wei, C.L., Yaci, K., Yamamoto, H., Zabarcos, E., Zhu, S., Zimmer, A., Hile, W., Bult, C., Grimes, S.M., Teasdale, R.D., Liu, H.T., Smid, D., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kao, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Inamura, K., Itoh, M., Kao, T., Kawaji, H., Kawagishi, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Niinomiya, N., Nishio, T., Okada, M., Plas, C., Sibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanuki, A., Okamura-Ono, Y., Suzuki, H., Kawai, J., and Hayashizaki, Y.
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COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://fantom.gsc.riken.jp/.
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LILQRNGLKKFKVLMKTMNSSELTQDVLNSLNHSYDRTCAWEISLVLINSSNM LTSVSPFLCPKPKVQVLDLNNRNTSIPKDVTHQALOBNVNSLTDLPGCGRAFSSL SUVLFDNSVPSSEDFQCSQNRSUFTAGNNPQCTBLRDPVQFVNGWREVEVG SVKLFQFWFPRVEPVYLNLTNTTIRETREFETSETALKSLMIEHVNOVFLSKEA LYSFVAEMNIKMISDQTPTFHMCPQFPPSPSFFELNFQFVDFQFQGCFSSNL LILQRNGLKKFKVLMKTMNSSELTQDVLNSLNHSYDRTCAWEISLVLINSSNM LTSVSPFLCPKPKVQVLDLNNRNTSIPKDVTHQALOBNVNSLTDLPGCGRAFSSL SUVLFDNSVPSSEDFQCSQNRSUFTAGNNPQCTBLRDPVQFVNGWREVEVG SVKLFQFWFPRVEPV

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Qy	241	ATGCTCTAGAACATACATGCTAGCTCAGGCTCTGACAGCAGCTTCTACAGAGTTG	300	Qy	1321	AGACATAAGAAACTGCACTGGTTGAGATAGTGGTTAAATTGCTCAAT	1380
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Qy	481	TGTAAGAATTTGGCAACTTATCACACTGAAATTCTGGATGAGCTGATGAAGCTG	540	Qy	1561	GTATTGATCATCACAACTTCACTGTTCCATCCATCTGAGGTTCTCAGGCT	1620
Db	535	TCTAAGAATTGGCAACTTACAGGCTGAGCTGAGCTGAGCTGCAAGATTC	594	Db	1615	GTGCTGTCATGACCATACTCAGTTCCATCCATCTGAGGTTCTCAGGCT	1674
Qy	541	CTAAATAGATTGCTGCCAATGCTCACTGCACTAACTTCTCTGGATTA	600	Qy	1621	CAGAAGTAGGGCATAAAGCAGGGACATCCATGTCAGCTACAGTCAGTC	1680
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Db	775	GTTTGGACATTTACACTGAGTAATTAAATTGATGAGAAACTGTCAGGTA	834	Db	1855	CCACTGCCTGTGACTACTGTTGCTGAGCTGTCACCATCGGGCCTACTATGCTG	1914
Qy	781	ATTAATTTTATCAGAACTCACCTAACCTACTGAAATTCTACCTCAACCAC	840	Qy	1861	GCTGAGCTGACTCCCTCTGCTCATCTACTGTTGATCTGCTGCTGCTG	1920
Db	835	ATGACATTTTCTCAGAACTTACACCAAGGGTCCACCTTATGACCTG	894	Db	1915	GCTGTCATCTGGGCTTCCCTGTGCTCTACTTGTGACCTGCTGTTGAGTGTG	1974
Qy	841	ATGAAACAGCTTGGAAATGCTGGCTGAGGCTTCAATTCTTGGCCAAACCTGT	900	Qy	1921	TGCCAGTGGCCAGACCTGCGGAGGGCCAGGAACATACCCCTAGAGAACTCCAAGA	1980
Db	895	ATGAAACACCTGGAGTGTCTGGTTAACCTTCTGACCTG	954	Db	1975	TCTCAGGAGACAGCAGCAGGACAGGACATCCCTTGTAGAGAACTCAGAGA	2034
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Db	1015	TACTCGGAGACGACTGACTGAGCTGAGCTGAGCTGAAACACAGTGTCTC	1074	Db	2095	GAATTACTACCAACTAGAGAACTGACATCCGGTTGCTCCATGAGGACTT	2154
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RESULT 4
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DEFINITION Mus musculus TLR6 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY16999
VERSION AY16999.1 GI:39772959
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Puteleostomi;
Mammalia; Eutheria; Eucrocotylires; Gliria; Rodentia;
REFERENCE Sciuorognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2388)
Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBLMED 14717302
REFERENCE 2 (bases 1 to 2388)
AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES LocationalQualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>2388
/gene="TLR6"
/locus_tag="HOM6077"

ORIGIN

Query Match 55.4%; Score 1525; DB 14; Length 2388;
Best Local Similarity 77.6%; Pred. No. 0;
Matches 1845; Conservative 0; Mismatches 532; Indels 0; Gaps 0;

QY 67 ATGACCAAAGCAAGAACCTATTGTTAAAGCTTCATTGTGTTGCCTTATGATA 125
Db 1 ATGAGCCAAGACAGAACCTATCGTGGGGTTCCATTGTGTTGCCTTGGCTTA 60
QY 127 ATAGTGGACAGAACATTGACCTCGGACGGAATGAAATTGAGCTAGAACGTC 186
Db 61 ATAGTGGACAGAACATGACCCCTTCTTAATGAACTGTGATGTTACATCAAC 120
QY 1087 ACACCTTATAACATGCTGTGCTCATGCCAACAGCATCGATGTTGACATT 1146
Db 1021 ACCCTTCTCATCACATGGTGGCCCATCCCCAACGCTCATTTACATTCTGACATT 1080
QY 1147 ACCCAGAACGTTTACAGAGTAGTATTGAAATGTTCCACCTTGTAAATTGAG 1205
Db 1081 ACCCAGAACGTTTACAGAGTAGTATTGAAATGTTCCACCTTGTAAATTGAG 1140
QY 1207 ACACCTTCTACAAAAATGATAAGACCTTCAAGTAGGTCTCATGAGG 1266
Db 1141 ACACCTTCTACAAAGGATGTTGAGAAGACTTTCATGAGTCAAG 1200
QY 1267 GATATGCCCTTGTGAAATGAGCTGTGAGATCTTGGATCTGGAGACAT 1326
Db 1201 AATATGCTCTCTGAACTTGGATGTTGAGTCTTGTGAACTCTCAT 1260
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Db	1321 ACAGGCCTCTCTCTAGATGCTTACCTCCAGGTCAGCTCAAGCACAC 1380
QY	1447 AAATAAAGGCGTCTAACAGGCTAAATGGAAATGGAGCTTGAGAACTCATGT 1506
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Db	2041 GCGAAGAGCATGGAGAACATCATCAATTCTCATGAGAGACTACAGGCCCTT 2100
QY	2167 GTTTGTCTCCAACCTGGCAGGTGGTGGTCCATTAGAACGACTCTTGTCCAT 2226
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CNSRTRM	
TITLE FANTOM Consortium	
JOURNAL Functional annotation of a full-length mouse cDNA collection	
PUBLMED 11217851	
REFERENCE	
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osoyo, N., Saito, R., Suzuki, H., Yamamoto, I., Nikaido, T., Osoyo, N., Saito, R., Suzuki, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nozaki, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.R., Bult, C., Bult, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batyalov, S., Schriml, L.M., Bredt, D., Brusic, V., Chohtia, C., Corbani, L.E., Cousins, S., Della, E., Dragani, T.A.,	
RESULT 5 AK154253	
LOCUS AK154253	
DEFINITION 2522 bp mRNA linear RT-PCR 21-SEP-2005	
RECEIVED AK154253	
MATERIALS AND METHODS Mus musculus NOD-derived CD1c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630012B11 product:toll-like receptor 6, full insert sequence.	
REFERENCES AK154253.1 GI:74178406	
KEYWORDS HTC; CAP trapper.	
SOURCE Mus musculus (house mouse)	
ORGANISM Mus musculus	
Bukaiyota; Metzoco; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buttoeria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE 1 Carninci, P. and Hayashiaki, Y.	
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kondo, H., Okazaki, M., and Hayashizaki, Y.	
TITLE High-efficiency full-length cDNA cloning	
JOURNAL Meth. Enzymol. 303, 19-44 (1999)	
PUBLMED 10349636	
REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kondo, H., Okazaki, M., and Hayashizaki, Y.	
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kondo, H., Okazaki, M., and Hayashizaki, Y.	
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)	
PUBLMED 11042159	
REFERENCE 3 Shibata, K., Kondo, H., Okazaki, M., and Hayashizaki, Y.	
AUTHORS Shibata, K., Kondo, H., Okazaki, M., and Hayashizaki, Y.	
TITLE Genome Res. 10 (10), 1617-1630 (2000)	
JOURNAL JOURNAL OF CLONING TECHNOLOGY 2000	
PUBLMED 11076861	
REFERENCE 4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kondo, H., Adachi, J., Fukuda, S., Arakawa, T., Izawa, M., Nishii, K., Kiyosawa, H., Kondo, S., Yamamoto, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, Y., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Quackenbush, J., Schriml, L.M., Stabili, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Pirunno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hoffmann, M., Hume, D.A., Kanoji, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, Y., Schonbach, C., Seva, T., Shiba, Y., Storch, F., Suzuki, H., Toy-ko-oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wysham-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S., and Hayashizaki, Y.	
TITLE RIKEN Genome Exploration Research Group Phase II Team and the RIKEN Genome Exploration Research Group Phase II Team and the	
JOURNAL Nature 409 (6821), 685-690 (2001)	
PUBLMED 11217851	
REFERENCE 5 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osoyo, N., Saito, R., Suzuki, H., Yamamoto, I., Nikaido, T., Osoyo, N., Saito, R., Suzuki, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nozaki, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.R., Bult, C., Bult, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batyalov, S., Schriml, L.M., Bredt, D., Brusic, V., Chohtia, C., Corbani, L.E., Cousins, S., Della, E., Dragani, T.A.,	

REFERENCE	CONSRM	JOURNAL	COMMENT		
AUTHORS	TITLE	PUBMED	TITLE		
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gribble, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gutinich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maitais, L., Marchionni, L., Mikl, H., Nagashima, T., Nunata, K., Okido, T., Pavani, W.J., Pertea, G., Pesole, G., Perlovsky, N., Pilati, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, J.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arkawa, T., Fukuda, S., Hara, A., Hashizume, W., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.	Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlstedt, C.	Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlstedt, C.			
CONSRM	FANTOM Consortium	16141073	RIKEN Genome Exploration Research Group		
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	12466851	Antisense transcription in the mammalian transcriptome		
REFERENCE	Nature 420 (915), 563-573 (2002)	12466851	Science 309 (5740), 1564-1566 (2005)		
AUTHORS	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Balalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impiombato, A., Apweiler, R., Aturalia, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Berzano, T., Bono, H., Chalk, A.M., Choi, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Paulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Fukao, S., Garibaldi, M., Georgii-Hemming, P., Gigerer, T.R., Gojobori, T., Green, R.E., Gutinich, S., Hachter, M., Hayashi, Y., Henrich, T.K., Hirokawa, N., Hill, D., Humannicki, L., Iacono, M., Iwano, A., Ishikawa, T., Jakk, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kels, J., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madra, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Minrone, P., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakuchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavani, W.J., Pavesi, G., People, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Selzberg, S.I., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sesha, L., Sheng, Y., Shibusawa, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiyama, K., Sutcliffe, R., Takenaka, Y., Taki, K., Tammaro, K., Tan, S.L., Tang, S., Taylor, M.S., Tedmer, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamamoto, H., Zabarcovsky, E., Zhu, S., Zimmer, A., Hida, W., Butt, C., Grimmold, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlstedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arkawa, T., Iida, J., Immamura, K., Itoh, M., Kato, T., Kawabata, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Nitomiya, N., Nishio, T., Okada, M., Plessy, C., Shibusawa, Y., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.	8 (bases 1 to 2522)	The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ , Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	12466851	Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://fantom.gsc.riken.jp/ , Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
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JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	12466851	Location/Qualifiers	cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
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JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	12466851	FEATURES source	1. /organism="Mus musculus" /mol_type="mRNA" /strain="NOZ" /db_xref="FANTOM DB:F630012E11" /db="XREF" /taxon=T0090" /note="putative toll-like receptor 6 (MGI MGI:1341296 GB BC055366, evidence: BLASTN, 99%, match=2490)" Location/Qualifiers	1. 2522
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Qy	302 CAGTTTGACACTTCCATACAGATCCGCTACTTGATTAAAGTTTCAGTTCA 361	Db	1407 ATGCTTACAGGCTCTGCTTCAGAATCTTCAAGTCAGTCCTGTACAC 1466
Db	327 GAGTTCTGAGCTCTCCACACAGATACTGGCTTGAATTCAGTATCTGTCA 386	Qy	1441 AGCAATAAAATAACAGGCTTCAAACAGTAACTGGAGCTTGCAAGAAC 1500
Qy	362 ACCGAGATTAGATAATTGGATTAACTCTATAGTCAGTCAGAACAGATACT 421	Db	1467 AACAGGAGATAATGAGCATCCAAAGATGTCACCCACCTGAGGCTTG 1526
Db	387 ATCAGGACTTAGAAATACCTGGATGTCACCAACTGGTGCAAAACATCT 446	Qy	1501 ATGTTGCTTCATACTTAACTGACCTTCCAGCTTCTGGAGCTTGTGAG 1560
Qy	422 CTATTTGAGTTTCAGGATTAGATCTCTATCGATGTTCAAGGCTTGCCCAC 481	Db	1527 AATGAGCATCCAACTCTTAAGCTGACTCTCTGGGGCTTCAGCACCT 1586
Db	447 CTATGCCGAGCTGAGGCATCTAGACCTCTCATGACTTGTGACTGCTGT 506	Qy	1561 GATTCATGATCTGATCACATTCACTTCCACCATCGCTGATTTTCCGAG 1620
Qy	482 GTCAGGAATTGGCACTTACACACTGAAATTCTGGATGTCAGTGTGCTGC 541	Db	1587 GTGCTGTCATCGACCATACTCAGTTCCATCCTCTGAGGATTTCAGT 1646
Db	507 GTCAGGAATTGGCACTTACACACTGAAATTCTGGATGTCAGTGTGCTGC 566	Qy	1621 CAGAAGTAGGCTATAAAAGCAGGGACATCCATGATGACCTGAGTA 1680
Qy	542 AAAATTAGATTTGTCGCCAAATGCTCACTTGCACTTAAGTATATCCTTG 601	Db	1647 CAGATATAGATCCCTAACAGGGAAAGAACCCATTCACATGAGCTG 1706
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Qy	602 GAAATTATATAAAGAATGAGACAGAAAGTCACAAATTCTGAATGCAAAACC 661	Db	1767 GACTTGTGACAACTAGCTGGTAGCCAGAGAAGTGTGGGAGGGCTG 1766
Db	627 TGGATTTATGATGAGACAGAAAGTCACAAATTCTGAATGCAATGAGCT 686	Qy	1741 TATAAGTGTACTCCAGAAAGTATAGGAGAACCCACTAAGGACTTCAGT 1800
Qy	662 TTCACCTGTTTCCCAACTAGTTATTCGATTCAGTGAATCATGAACTG 721	Db	1767 TACAGGTGACTACAGCTAACAGTCACTGAGTGTAGAGGGCTGGCTGAT 1740
Db	687 TCCATTTGTCCTTCACAAATAGCTGTCCTGTCAGTGAATGTCAG 746	Qy	1801 GAATTATCCTGACACATAACTCTGCTGATGTACCATGTCGGCACATG 1860
Db	722 CTTAGGGTGTACACTGACTAATTAATTAAATGATGACACTGTCAGTTCA 781	Db	1827 CCACCTCTGTGATRACTGTCGACTGTCGACTGTCACCATCGGGCA 1886
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Db	782 TAAATTATTCAGACTCACCAGAGGTAACTCTACTGAAATTACCTCAACCA 841	Db	1887 GCTGTCAGTCTGGCTTCTCTGTCCTACTTGTGACCTGCTGTGTG 1946
Db	807 TGACATTTTATCAGAACTCACCAGAGGTCCACCTTATGAGTGTGAC 866	Qy	1921 TCCCACTGGACCAAGACTCGGGAGGGAGAACATACCCCTAGAGA 1980
Qy	842 TAGAACAGACTGTGAAATGCTTGTGAGACTTCTGAACTTCTGGCAAC 901	Db	1947 TGTCACTGGACACAGACCAAGCAGCACGGGCCAGGCATCCCTGAG 2006
Db	867 TAGAACACACTGGAGTGTCTGGTTAACTTTCCATTTTGGCCCGACCG 926	Qy	1981 AACCTCCAGTTCTGCTTTTATTCTATAGTGACCATGATCTGCTGG 2040
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Db	1047 TTTCACAGAGGGCGCTATACCTGGTTGTGAGTGAATCATGTCCTACT 1106	Qy	2161 ATCTTGTGTTGTCCTCCAACTTGTCAGAGTGTTGGGCCATTA 2220
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Qy	1142 ACTTACCAAGAACGTTCAAGATAGATTTGAAAMGTTCCACGTGTTAAAT 1201	Db	2247 GCCCATCATACCTCTCTCATGAAAGCTTCACTTACTCTCATCTG 2306
Db	1167 ACTTACCAACGATGTTACTGACAGTGTGTTGGCTTCACTTAAGAGAT 1226	Qy	2281 ATTCACAGACAGCTCCACACAGTACACAGAGCTGAGGCTCTGACCCAG 2340
Qy	1202 TGGAGACACTTCTTCAAAAGGATTAAGGCTTCACTGCTGCTGCTG 1260	Db	2307 ATTCACAGACACATTCCTGGCTGAGTACACAGAGCTTGGCTCATGG 2366
Db	1227 TGGAGACACTTCTTCAAAAGGATTAAGGCTTCACTGCTGCTGCTG 1286	Qy	2341 ACTTATGTCAGTGGCCCAAGGAGAAAGAACCGTGGGCTTGGCTAC 2400
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Db	1347 GCATGAGACAGGACATGGCTGGCTGGCTGAGGATATGAGTGTGACT 1406		
Qy	1381 ATGCTTACTGACTCTGTTTACCTCCAGGATCAAGGACTCTGATCTCAC 1440		

HSM80268	HSM80268	2806 bp	mRNA	linear	HTC	20-JAN-2005	Db	275	ATGACTAGCATTTCCATTTCATCTCATGTAATCTTCGATCGAAATCAA
LOCUS	Homo sapiens		cDNA	DKFZP564I0682	(from clone	DKFZP564I0682).	Qy	148	TTCCTCCACGGAAATGATGTTAGTCAGTGACAGTCATAAAGGGCTTATTCTGTTC
DEFINITION							Db	335	TTACCTGAGAAGTGAATTCTAGTGATAGTCATAAACGGTCATCCACGTTCT
ACCESION							Qy		394
VERSION	All05262.1	GI:4886482					Db		
KEYWORDS	HTC.						Qy	208	AAAGACCTACCCCTGAAACCAAGTGTAGTATCTCTCAGACACTCATCCTGACCT
SOURCE	Homo sapiens	(human)					Db		267
ORGANISM	Homo sapiens						Qy	395	AAAGACCTATCCAGAAACAAACATTTATGCAAATTATCTGACTT
REFERENCE							Db		454
AUTHORS	Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellemeier,R.,						Qy	268	CAGGTCTGAGATGAGCTTCTATCAGTGAGTGCACGTTGAGACTTCCTACAAQGA
COMMENT	Neuberberg, GERMANY						Db		327
RESEARCH CENTER	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;						Qy	455	TGGACTCTGACATCTATCAGTCACAACTGAGGTTGATAATTCTCATATA
SEQUENCED BY	sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZP564I0682) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:						Db		514
JOURNAL	http://www.rzpd.de/cgi-bin/products/cl.cgi?clonedB=DKFZP564I0682						Qy	328	ATCCAGTACTGATGTTAGTGTAGTTAGTGTAGATTTGGATTA
DIRECT SUBMISSION	Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.						Db		387
THE GERMAN cDNA CONSORTIUM	Location/Qualifiers						Qy	515	ATCCAGTACTGATGATCAGTGTTQAATCACAGGAGTTGGATCTGGATTG
Submitted (20-JAN-2005)							Db		574
Neuberberg, GERMANY							Qy	388	TCTCATATCATCTGCAAAAGTATCTGCCATCCATTGCTGAGTCAGGCTT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;							Db		634
sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZP564I0682) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:							Qy	448	CTCTCATCAATGATTCAAGCCCTGCCATCTGAGGATTGGCACTTCAA
http://www.rzpd.de/cgi-bin/products/cl.cgi?clonedB=DKFZP564I0682							Db		507
FURTHER INFORMATION ABOUT THE CLONE AND THE SEQUENCING PROJECT IS							Qy	635	CTGTCATTAATGCTGATGTCCTCTATGAGAAGTGTGCAATATGCTCAA
AVAILABLE AT http://mips.gsf.de/projects/cdna/ .							Db		694
LOCATION/QUALIFIERS							Qy	508	CTGAAATTCTGGGTTGAGCACACACACTAGAGAAATCTAGTGTGCTGCAAT
FEATURES							Db		567
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	/organism="Homo sapiens"						Qy	695	CTAAATTCTGGGTTGAGCACACACACTAGAGAAATCTAGTGTGCTGCAAT
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	/clone="DKFZP564I0682"						Db		627
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	/clone_id="564 (synonym: hfbr2). Vector pAM1; host						Qy	628	ACAGAAAGTCTACAATCTGATGAAAAACCTCACCTGTTTCAACCAACTAGT
	X1-2806; sites NotI + SalI"						Db		687
	/dev_stage="fetal"						Db		815
	/note="tol-like receptor 1"						Qy	688	TATTCCTATTCAGCAAGTCTAGTGTAACTTCTGTTCTACAATCTGACTAAT
	1. -2806						Db		747
	/gene="DKFZP564I0682"						Qy	688	TATTCCTATTCAGCAAGTCTAGTGTAACTTCTGTTCTACAATCTGACTAAT
	275 . -2635						Db		747
	/gene="DKFZP564I0682"						Qy	688	TATTCCTATTCAGCAAGTCTAGTGTAACTTCTGTTCTACAATCTGACTAAT
	/codon_start=1						Db		934
	/product="hypothetical protein"						Db		934
	/protein_id="CB43164.1"						Qy	748	ATTAAT-----TGAATGACAACTGCAAGTTCTAATTTTATCAGACT
	/db_xref="GI:886483"						Db		801
	/db_xref="GO:Q03399"						Qy	935	ATCAAAATGCTGCTAGAGATGAAATGTTCTCTAACTGAACTGAACT
	/translation="MTSIFIFAIPLMILQIRIOLSEERFLVRSRKGQLIHVKDLS						Db		994
	OKTTLINSQYISLSDILSKURKILWPKRICKFNSQKFLGSTTHAKSSLTPLIA						Qy	802	ACAGAGGTCACTTACTGATTTACCTCACACACATAGAAAGACTGGAATGC
	NKLVKLSCHEPVNLKHDLSFNFAFLPAVLPKQVKEFVNLKQVKEFVNLKQVKEF						Db		861
	HNLNSKVLUVGETGEKEPGQDENTESLHVPTKEFVHLDSVKTVALE						Qy	995	AAACAAATCCAAGTATCACGTCACGTTAACACATGAAACACTGAACTGAACT
	SNIKQVLLEDSKCSFSLILAKLQKPLKLISETLWTFNLSFRQWHTTWYS						Db		1054
	SISVYKLGQDGRDFPDSLSQTSKLALISQVQVSVDFGPQSYTEFISNQKNTVVS						Qy	862	CTGGCTGAGCTTCTGCCAACCTGTTGGATATCTCAATATTAACT
	GTRMMHMLPSKIPRFLPHDLSNLLDTDFENGHLETELTLQMONLKELSKIAE						Db		921
	MTTOMKSLQDLSQNSVSYDKEGCDWSKWLSSLNMSNLIDITFRCCLPKVAD						Qy	1115	CTGAGACTGCTAGGTCTGCTGACTTCAGATTTCTGACTCTCTGAG
	DHKHKKIKPQVKEFVNLKQVKEFVNLKQVKEFVNLKQVKEFVNLKQVKEF						Db		1114
	FFOCOKMSKIKADNPFOOTCEGEGFKVNDLQVSEVLEGPSYKQDYPESRGT						Qy	982	GCATGCACTAGAAGATACGAAACAGTTCTGTTCTAGACAGACGTTGAC
	LKDPMELSLSCNTIVVATMLAVVNTSGCILDFWJLNRVCOMTORRR						Db		1041
	NIPPELQRNLQFHAFITSQGHDFWJKLPLPQKMGQICHERNVCPIVGSIVEN						Qy	1175	GCCTCTCTATCACGACTGTTGAGCTGTTGAGCTTACCTTACAC
	ITTEKSYKSIPLVSPNPFYOSECHYELFAHNHLFHGSNSLILLEPIQYSIP						Db		1234
	SSYHKLKSIMARRTYLEPEKSKRGLFWANLRAINLKTEQAKK"						Qy	1042	ACCGTGTCTTCTGAGATGACATTAATGTTGACCTTACATGAGACTTAC
ORIGIN							Db		1294
Query Match	52.3%	Score 1439.4;	DB 6;	Length 2806;			Qy	1102	ATGCTGTTCTCATGCCAGCACTCAGTTTGACTTACCCGAACTGTT
Best Local Similarity	76.2%	Pred. No. 0;					Db		1161
Matches	1786;	Conservative	0;	Mismatches 551;	Indels 6;	Gaps 1;	Qy	1295	ATGCTTGCCTACATCCAAATGACCGCTTCTGCAATTCTCTA
OY	88	ATGTTAAAGCTCCATTGTTGCTTGTGATCTAATGTTGAGACAGAATCCAG	147				Qy	1162	ACAGATGATGTTTGTGAAATGTCACGTTGAGACTTAC
							Db		1221
							Qy	1355	ACAGACCGGTTTGTGAAATGTCACGTTGAGACACTTAC
							Db		1414

QY	1222	AAGAATGGATAAACGCTTCAAGTAGTCATGAGAAGGATTCCTCTTG	1281	2302	AACAGTACCAAGCTGAGGCCTCATGAGCAGGACTATTGGAGTGGCCAG	2361
Db	1415	ATGAAATCAATTAAGAACCTTCACAATAGTCGAATGACTACAGATGAGCTCG	1474	2495	AGCAGTTATCACAAAGCTCAAAGTCCTATGCCAGGAGCTATTGGATGGCCAG	2554
QY	1282	GAATATCTGGTGTGCTGAAATTCTGGAACTACATAAGAAACTGCACT	1341	2362	GAAAAGCAACGCGGCTTCTGGCTAACATAGGCCGTTATATGAAATTA	2421
Db	1475	CAACATTTGGATATTGCCAGAAATTGTGAAGCTATGAAAGAAGGAGCTTC	1534	Db	2555 GAAAAGCAACGCGGCTTCTGGCTAACATAGGCCGTTATATGAAATTA	2614
QY	1342	TGGGTGAGAGTATAGTGCTTAATTGCTCAATATGCTTAATGACTGTTTC	1401	QY	2422 ACA 2424	
Db	1535	TGGACTAAAGTTAAATTGAGTTAAATGCTCAATATGCTTAATGACTGACTTC	1594	Db	2615 ACA 2617	
QY	1402	AGAAGTTACCCAGGATCAAGGACTTCATCTCACAGCAATAAGACGT	1461	RESULT ?		
Db	1595	AGATGTTACCTCCAGGATCAAGGACTTCATCTCACAGCAATAAGACGT	1654	DY109015		
QY	1462	CCTAAACAGTGTAACATCGAAGCTTGCAGAAACTCAATGTTCTTAA	1521	DY109015		
Db	1655	OCTAAACAGTGTAACATCGAAGCTTGCAGAAACTCAATGTTCTTAA	1714	DEFINITION	DY109015 bp mRNA linear EST 01-FEB-2006	
QY	1522	ACTGACCTCTGGATGCGAGCTTAGGCCTTCTGATGATCATGATCAAT	1581	ACCESSION	DY109015.1 GI:86272292	
Db	1715	ACTGACCTCTGGATGCGAGCTTAGGCCTTCTGATGATCATGATCAAT	1774	VERSION		
QY	1582	TGAGTCCCACCATGGCTATTCAGAGCTGCCAGAGATGCAATAAA	1641	EST.		
Db	1775	TGAGTTCACCATGGCTATTCAGAGCTGCCAGAGATGCAATAAA	1834	BOS TAURUS (cattle)		
QY	1642	GCAGGGGACATTCATCCAAATGACTCTGAGCTAGAGAATTGTCAAATAATAGAC	1701	ORGANISM		
Db	1835	GCAGGGGACATTCATCCAAATGACTCTGAGCTAGAGAATTGTCAAATAATAGAC	1894	Mammalia; Bovidae; Bovinae; Bos.		
QY	1702	CAAGATCAGTGAGTGTAGAGGCTGCTGATCTTAATGTTGACTACCAGAA	1761	PECARIA; BOVIDAE; BOVINE; BOVUS.		
Db	1895	CAAGATCAGTGAGTGTAGAGGCTGCTGATCTTAATGTTGACTACCAGAA	1954	1 (bases 1 to 351)		
QY	1762	AGTATAGAGGAGCCACTAACGACTTCATGCTGAATTACTGACATACT	1821	McClurkin, A., Wilson, T., Molenaar, A., Grigor, M., Davis, S.,		
Db	1955	AGTTATAGAGGAACTACTAAAGGTTCACTCTGATAATTACTGCAACAACT	2014	Glehn, M., Havukkala, I., Watson, J., Crawford, A., Wheeler, T.,		
QY	1822	CTGCTGATCGAACCTATGGCACCATGGTGGCACCATGGTGGTGGTGGTGG	1881	Hagmann, L., Lee, R., Heil, W., Johnstone, P., Macbooi, N., McMahon, C.,		
Db	1882	TGCTATCTACTTGATCTGGCTCTGGTACTCGAGATGCTGACCTCCCTC	1841	McCracken, J., Stilwagen, K., Farr, V., Singh, K., Whitley, J.,		
QY	2075	TGCATCTACTTGATCTGGCTCTGGTACTCGAGATGCTGACCTCCCTC	2134	Nicholas, K., Savin, K., Mather, A., McPartlan, H., Whitley, J.,		
Db	1942	CCGAGGCCAGAACATACCTTAGAGAACCTCAAAAGACCTCCAGTT	2001	Wells, M., Bowman, P., Goddard, M., Langford, C., McEwan, J. and		
QY	2135	CGCAGGCCAGAACATACCTTAGAGAACCTCAAAAGACCTCCAGTT	2194	Atkinson, P.		
QY	2002	ATTCTATATAGAACATGATCTGGCTGGTAAAGTGAATTGGTACCTAACAGAA	2061	AgResearch, Genesis and Primary Industry Victoria Bovine EST		
Db	2195	ATTCTATATAGGGCAGATCTTCCTGGTAAAGTGAATTGGTACCTAACAGAA	2254	Project		
QY	2062	AAAGAGATATACAGATGCTTCATGAGGGAACTTGCCCTGCAAGAACATG	2211	Unpublished (2006)		
Db	2255	AAAGAGGTATACAGATGCTTCATGAGGGAACTTGCTCTGCAAGAACATG	2314	Contact: Macpool N.		
QY	2122	AAAGATATACACTCATGAGAGTACAAGTCATCTTGTGCTCCAC	2181	AgResearch Ltd.		
Db	2315	AAAGATATACACTCATGAGAGTACAAGTCATCTTGTGCTCCAC	2374	Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,		
QY	2182	TGTGTCAGAGTGAGCTGCTGCAATTAGAACCTTACAGTCATCAATCTCTCAT	2241	Email: nauman.macpool@agresearch.co.nz.		
Db	2375	TGTGTCAGAGTGAGCTGCTGCAATTAGAACCTTACAGTCATCAATCTCTCAT	2434	FEATURES		
QY	2242	GAAGAGTCTAATCACTTAATCTGCAAGAACCTTACAGTCATCAATCTCTCAT	2301	source		
Db	2435	GAAGAGTCTAATCACTTAATCTGCAATTAGAACCTTACAGTCATCAATCTCTCAT	2494	REFERENCE		
QY	2308	TTGACAGTTTGAGACTTCCTACATGTTCTCCAAACTATCCCTGAAACCACTTA	364	AUTHORS		
Db	2425	CTGAGATTGATATTCTCATATAGATCCAGTCTGACTGTTTAA	484	1		
QY	358	TCAACAGGATTAGATATTGGATTCTCATATAGTGTCAAAAGATATCTGC	417	KEYWORDS		
Db	485	TTCACCCAGGAACTGGATACTGGATTGTCACACAAATTGGAGAAGTTCTTG	544	EST.		

ORIGIN
Query Match: 46.0%; Score 1267.4; DB 10; Length 3051;
Best Local Similarity 73.0%; Pred. No. 1.8e-302;
Matches 1644; Conservative 0; Mismatches 601; Indels 6; Gaps 1;

QY 178 AAGTCAAAGGGCTTATTCATGTTCCAAGAACCTACCGCTGAAACCAAGCTTA 237
Db 305 AGTCACAAAGGGCTTACATGTTCCAAGAACCTACCGCTGAAACCAAGCTTA 364

QY 238 GATATGCTGAGACTACATGCTGAGCTGCTGAGCTGAGCTTCTGAG 297
Db 365 GATATGCTGAGACTACATGTTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 424

QY 298 TTGACAGTTTGAGACTTCCTACATGTTCTCCAAACTATCCCTGAAACCACTTA 357
Db 425 CTGAGATTGATATTCTCATATAGATCCAGTCTGACTGTTTAA 484

QY 358 TCAACAGGATTAGATATTGGATTCTCATATAGTGTCAAAAGATATCTGC 417

Db 485 TTCACCCAGGAACTGGATACTGGATTGTCACACAAATTGGAGAAGTTCTTG 544

Qy	418	CATCCATATGAGTTGAGCAATTAGATCTCATTCATGATTCAAGGCCCTCCC	477	Qy	1492	CGAGAAGTCAGTGTGTTCAATTCTTAAGTACCTCCMGGATGCGCAGCTTAGC	1551
Db	545	CACCCTACTCTCACCTAACCTCAAGCTAGACTAGCTCTCATTTAATCATTGATCCCTGCC	604	Db	1625	CAAGACTCAACCTGTCTCCATTCTTAA3CCACCTTCCTGATGTTGTACTTTC	1684
Qy	478	ATCTGTTAGGAATTGGCAACTTATCACACACGAAATTCTTGATGAGTCATTAAG	537	Qy	1552	AGCCTTCGTGATTGATCATGATCACGAAATTGTTCCACCCATGGCTATTTC	1611
Db	605	ATATGCCAGAGTTGGCAACATGTCTCACTAGAATTCTGGGGTGAGTGCACACAG	664	Db	1685	ACCTTCATCTGACATGACTAACTOAATTCCAACTCCATGCTTTC	1744
Qy	538	CYGCACAAAATATAGATTGTCGCAATGTCATCTGATCTAGTATATCTCTGAT	597	Qy	1612	CAGAGCTCCAGAGATGAGGGCAATTAASCGGGGACAATCATCCAACTGATCTG	1671
Db	665	TTCAGAAATTCCAGTGTGCACTGATCACTCTATGCACTGAGTTTATGTC	724	Db	1745	CAGAGCTCCAGAGATAGGTCCTCAAGGGGGACAACTCCATCCAAATGTTCTGT	1804
Qy	598	TTRAGAAATTATAAAGAAATCAGACAGAAAGTCAGAAATTCTGATGCAA	657	Qy	1672	GAGCTAGAGATTGCPAAAMATAGACCAAGTACAGTGAAGTTAGAGSCTGG	1731
Db	725	TTPAGGAGACTTATGGAAAGAGAGATGGCGGAGGCCTCAAGCTTAAGACAG	784	Db	1805	GAGCTAGAGACTTCATCCAAGTAATGGCCAGTATCAGTGACGTTGAGGCTGG	1864
Qy	658	ACCTTCACCTGTTTCACCAACTAGTATTCTCTATCAAGAAATATCGTT	717	Qy	1732	CTGATCTTAAAGTGTGACTACCCGAAAGTTAGAGAAGGCACTAAAGGACTT	1791
Db	785	AGTCTGACATGTTCCACAGGAAGGATTCATTATTGAGCTGTAGTC	844	Db	1865	CCTGAGCTTATAAGTGTGATCATCCGGAAGCTACAGGAAACCCCTCAAAGGTC	1924
Qy	718	AATACTTTAGTTGCTTACAATGACTAATTAAT-----TGATGAGACAATGT	771	Qy	1792	CACATGCTGAAATCTGCTGTTGATGAACTGTCGTTGATGATGATGGCT	1851
Db	845	GACACACAGTAGTCTGAGCTATCCAACTGTCATTATTGAGCTGTGAGTATGGCT	904	Db	1925	CAGGTATCTGAGCTATCTGCAACACAGCTCTGCTGATCATCACCATTGTTGG	1984
Qy	772	CTAGTTCTCATTAATTTCAGAACTCCAGAGGTCACTACTGATTAC	831	Qy	1852	CTGGTGTGCGCTGACTCTGACCTCTCCTGACACTCTGACTTGACACTCCGATTC	1911
Db	905	CTTATTTCGAAATGTCCTCAAACCTCAAAGACTCAAGTTCAACT	964	Db	1985	CTGGTGTGCGCTGCTGACTCTGACTTGCTCTGCTGATCTACCTGATCTGCCCCGTC	2044
Qy	832	CTCAACCACTAGAAACGACTCTGGAATGCTCTGTCAGAGTCTTGTGCCC	891	Qy	1912	AGGATGTTGCGAGCTGACATRACTCTGCTGATCGTCACTCCGTCGACATCCCTTAGAGAA	1971
Db	965	TTAACACACATGAAATRACTGTTGAACTCTCTTACAGATCTCCAGTTGGGT	1024	Db	2045	AGGATGTTGCTGAGCCAGACTCTGCTGATCGTCACTCCGTCGACATCCCTTAGAGAA	2104
Qy	892	AAACCTGTGGAATATCTCAATTACATTAATGAACTGTCGAGAAGAA	951	Qy	1972	CTCCAAGAAACCTCCGCTTCATGTTTATTCATACTAGTAACTGATGATCTGCTGG	2031
Db	1025	ACAAACATGAGACTCTCCATTCATGAACTGACAGTTACCTGACTCTGAGA	1084	Db	2105	CTCCAGAACTCTCCGTTCCATGCTTATTCATACTAGTGGGAGCATCTGCTGG	2164
Qy	952	GATTTACTTCTAAACGACATGAGATGACAACTATCGAACAA	1011	Qy	2032	CTGAAAGTGTGATTGATGTTACCTPAGAAAGAGATACTAGTTGCTTCATG	2091
Db	1085	GATTTGATTTCTGACACTCTGAGGCTTGTGTTACACAAAGTGTCCATG	1144	Db	2165	CTGAGAGATGATTAATCTACCTGAGAAAGATAATAGAATTGTCCTGAG	2224
Qy	1012	GTTTCTGTTTACAGACACTTGTGACCCGTTCTGAGATGAACTATGATG	1071	Qy	2092	AGGAACTTGTCCTGCAAGGATTTGTTTATTCATACTAGTAACTCATGATGAGT	2151
Db	1145	GTTTCACTGCTCCACAGGTTATGCTATATAATGTCATAATGAGACATC	1204	Db	2225	AGAACCTGTCGCTGAGGACAGCCGGCAGGAACTGCTGAGT	2284
Qy	1072	TTAACATTAGATACACCTTTACACTGCTGTCCTCATGCCATCCGAT	1131	Qy	2152	TACAGTCATCTGCTGTTGTCAGGAGCATTTGTCAGGAACTGCTGAG	2211
Db	1205	CTCACAGTGTCTGCACTGACATGGTCACATGTCGCTCCATGCCATT	1264	Db	2285	AGAACCTGTCGCTGAGGACAGCTGTCAGGAACTGTCAGGAGCATGTCGCTG	2344
Qy	1132	AGTTTTGAACTTACCCAGACGTTCAAGATGTTGAAAGATGTCACG	1191	Qy	2212	CTCTATTGSCCATCACAACTCTTCATGAGGACTTAACATTCATCTTCA	2271
Db	1265	CTGTTTGTGATTTCACAAATCTCTTACAGACAGCTTCAATACTGAAAT	1324	Db	2345	CTCTACTTTGSCCACCACAACTCTCTCCATGAGGATCTGATCTGATCTG	2404
Qy	1192	TAGTTAAATTGAGACACTTCTACAAAAAATGATTAAGACACTTCAAGTA	1251	Qy	2272	CTGGAACCCATCCAGAACAGAACGATTCCTAACAAAGTACCAAGAGTGAAGGCTCTG	2331
Db	1325	TGGCTTAAATTGAGACACTTCTACAAAGAAATGATTAAGACACTTCAAGTA	1384	Db	2405	CTGGACCCATCCAGAGTATCTGAGGATACCTCCAGAACGATGAGCTCTG	2464
Qy	1252	GGTCTCATGAGAAGGATATGCTCTGAAATCTGAGTGTGTTGAGTCTTG	1311	Qy	2332	ACGGACGGACTATTGCACTGCGCAAGAGAACGAAACGTCGGCTTTCGGCT	2391
Db	1385	GPTCATATGACGCCAGGAATGAGTCCTACAACTGAGTCGACATCCG	1444	Db	2465	GCACAGAACTTATGGAATGGCCCAAGGAGAGTAACACGGACTTTGGCT	2524
Qy	1312	GAATCTGTTGAGACATAAAGAAACTGACTCTGTTGAGATGTTGAGTAA	1371	Qy	2392	ACATTPAGGCGCTTTAATGAAATA	2422
Db	1445	ATGTAATGATGAGAAGGATGCGCTTGGCCCTGGCCGAAATTAAACTG	1504	Db	2525	AACCTAGAGCATCCATTAAACTGA	2555
Qy	1372	TCTTCATAATGCTTACTGACTCTGTTGAGATGTTGAGTAA	1431	RESULT 8			
Db	1505	TCTTCATAATGCTTACTGACTCTGTTGAGATGTTGAGTAA	1564	AK143721			
Qy	1432	GTCTCTCACGAAATAAAATAGAGCGCTTCAACAGAGCTGAAACTTG	1491	LOCUS	AK143721	3020 bp	mRNA
Db	1565	GTCTCTCACGAAATAACGATAGGAGATCCCTAAAGATGTCAGTCACTG	1624	DEFINITION			linear RTC 21-SEP-2005
				library	Mus musculus	6 days neonate spleen cDNA, RIKEN full-length enriched	
				sequence.		product:toll-like receptor 1, full insert	
ACCESSION				VERSION	AK143721	GI:74150781	

		Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M., and Hayashizaki, Y.
TITLE		
JOURNAL		
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC)', RIKEN Yokohama Institute; 1-7-22, Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: +81-45-503-9222, Fax: +81-45-503-9216)		
COMMENT		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/.
FEATURES		
source		Location,Qualifiers 1. -3020 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:F430012H09" /clones="F430012H09" /tissue_type="spleen" /clone_id="Riken full-length enriched mouse cDNA library" /dev_stage="5 days neonate" 1. -3020 /note="putative toll-like receptor 1 (MGP MGI:1341295 GB AF316985, evidence: BLASTN, 99%, match=2565)"
ORIGIN		
		Query Match 40.7%; Score 1119; 4; DB 6; Length 3020; Best Local Similarity 68.8%; Pred. No. 8; 5e-266; Matches 1571; Conservative 0; Mismatches 706; Indels 8; Gaps 2;
Qy		139 AGAATCCAGTCTTCGGAGGAATGAAATTCTAGTACAGACAAGTCATAAAGAACGCCAACCTTAC 592
Db		533 AAATCCATTATCTGGAGGTGAGCTTATCATAAAGAACGCCAACCTTAC 592
Qy		199 CATGTCCAAMAGACCTAACCGCTGAAACCAAGCTCTAGTATGTCAGRACTAC 258
Db		593 AGAGTGCCTAACAGGACCTAACCTTGCAAAACACTACTTTAGTCTATCACAAACATATA 652
Qy		259 GCTGAGCTTCAGGCTCTGACATGAGCTTCTACAGTGTACAGTTGAGACTTCC 318
Db		653 TGTGAGCTTCAGCTTGTGAACTCTCTCATGTCAGCTGAGGTTCTGATAATGTC 712
Qy		319 CATAACAAGAATTCAGCTACTCTGTTAGTGTCTTCAAGTCAACCGGAGTTAGATA 378
Db		713 TACAACAGACTCCAGTCTTATCATGTTTCAATTAAACAGAGCTGGATAT 772
Qy		379 TTGAGTTATTCATCAATCAGTCAGTCTTCTGAGTTCTGAGTTCTGAGCTTCC 438
Db		773 TTGGATTTGTCTCCACCHATGACCTTAAGGTCAGCTTGTGCCCCACAGTCAGCTCAAG 832
Qy		439 CATTAGATCTCTCATCAATGTTCAAGGCCCTGCCATCTGTAGGAATTGGCAC 498
Db		833 CATTGGACCTCTCTTAAAGCTTGTGACCTCCCTGACATGCAAAAGATTGGCAC 892
Qy		499 TATCACAACTGAAATTCTGAGCTGAGCTGAAATTAGATGTTGCTG 558
Db		893 ATGCCCAACTACAGTCCTGGTGTGAGCTTCTGGAGTCAAGTCAGTGTGAG 952
Qy		559 CCAATGCTCAGCTCTGCTCTAGTTATCCCTCTGGATTAGAAATTATATATAA 618
Db		953 CTGATGCTCATTTGAACTACAGTGAAGTTGCTGGTGTAGGAGATGCTTGGCAA 1012
Qy		619 GAAATGAGAGAGAAAGTCTACAATTCTGATGCAAAACCTTCACCTTGTTCAC 678
		Db 1013 AAAGAACCCGAACTCTTGGCAGCTTAGCAGACTCTGATATGTTTCCCG 1072
Qy		679 CCAACTGTTATTGCTTACAGTCAAGTACATATCAGTTACTTTAGGGCTTACAA 738
Db		1073 TGAAGAGGATTCGTTCTTCGGATGCTGTCCTGACACTAGATGGTTGAA 1132
Qy		739 CTGACTATATAAT-----TGAATGATGACAATGTCAGTTCTATTAATTAA 792
Db		1113 CTGCTCACATCTGGTGTGAGAACAGGGCTGCTTATTTCTAGTGTCTTG 1192
Qy		793 TCAGAACTCACCAGAGCTCACCTTACTGAAATTACCTCAACACATAGAACACT 852
Db		1193 TCAAGCTTGGAAAGATCTGAGCTTCAACATCTTACCCCTGAACTGTGAAACAG 1252
Qy		853 TGAATGTCCTGAGGTTCTGAGCTTCAAGGTTCTTCTGGATATCTCAAT 912
Db		1253 TGAATTCCTCTTATATCTCCAGATCTTGGCATTTGCCATTCAGTCAATTTCTCA 1312
Qy		913 ATTACATTACAAATTAATGGAAGCAATCTGAGAGATTCTTCTAAACAG 972
Db		1313 ATTACATTGAGGCTACAGTCAGCTTCAACATCTTACCCCTGAACTGTGAAACAG 1372
Qy		973 ACATGAAAGGTGAGCTACAGTCAGCTTCAAGGATCTGAGTTCTTCTACAGACA 1032
Db		1373 TCTCTGAGGCTTGTGATCATCAGTCTGAGTTCTGAGGATGTTCTGATCTCCCAGT 1432
Qy		1033 GCTTGTACACGGTTCTGAGTGAACATATGATGTTACCATTCAGTACACCT 1092
Db		1433 TACATATACATPATCTTGCATATGAACTCCAACTTACAGTGTGAAACAC 1492
Qy		1093 TTATACACATGCTGCTCATGCACCAAGCACATCTCAAGTTTGAACCTTACCG 1152
Db		1493 ATGGTCCACATCTGCCCCGTCCTCCAGTTAGCCATTCTGCATGTGGACTTACAGAT 1552
Qy		1153 AACGTTTCAAGATGTTGAAATGTCACAGTTGTTAACTGAGACTT 1212
Db		1553 AACCTTTTAACTGAGCTGTTTAAGACTGTTAGATTGAAACATT 1612
Qy		1213 ATCTACAAAMATGGATAAAGACCTTCAAGTAGGCTCTGACAGGATG 1272
Db		1613 ATTTACAAAGAATGTTAGTAAACCTGAGTAAACACTCTGAGATATCTGACATGCAAGATG 1672
Qy		1273 CCTCTCTGGAAATCTGGTTAGCTGGATTCTTGGATCTCTGACAGGATG 1332
Db		1673 ACATCCCTACAAACTAGTACATTACGAGTTCTGAGTAACTCTGAGATATCTGACATGCAAGATG 1732
Qy		1333 AACTGACTTGGTGTGAGACTATCGGTGTTAAATTGTCCTCAATATGTTACTGAC 1392
Db		1733 CCATGCCCTGGACCCAGAGTTGTTAGTTAAATTGTCCTGAGTATGCTTACGG 1792
Qy		1393 TCTGTTCTAGGTTACCTCCAGGATCAGGACTCTGATCTCAGCAGATA 1452
Db		1793 TCTGTTCTAGGTTACCTCCAGGATCAGGACTCTCAGCAGATA 1852
Qy		1453 AAGAGCTTCTAACAGTGTAAACTGAAAGCTTGTGAGACTCAATGTTGCTTC 1512
Db		1853 ATGAGCTCCATTAGTGTACCTCCAAAGTCAGGTTCTCCAGCCTTCAACAGGATA 1912
Qy		1513 AATTCTTTAATGACTCTTCGGATCTGGAGCTTGTGAGCTTCTGATTGATCATT 1572
Db		1913 AACTCTCTAACAGTGTACCTCCCTTCTGAGTTCTGCTGGTAC 1972
Qy		1573 GATCACATTGATTCACCTGAGCTTGTGAGCTTGTGAGGACTCTAATGAGTGG 1632
Db		1973 GACCATTAACCTGTTCCACCTCTGAGATGTTCTGAGATTTGAGATTTGA 2032
Qy		1633 TCAATAAAAGGGGGCAATTCATTCAATGTTCTGAGCTTGTGAGGTTGTCATAA 1692
Db		2033 TCCCTACAGGGAAACACCTTCATGCAATGTCAGTGTGAGGACTTGTGTCAG 2092
Qy		1693 AATATGACCAAGTATTCAGTGAAGTTGAGGGCTGCTGATCTTATAGTGTGAC 1752

FEATURES	SOURCE
Qy 1753 TACCCAGAAAGTTATAGGAGAAGGCCACTAAGGACTTCACATGTCGAATTATCTGC 1812	Db 2093 AACATAGCTGGTAGCAGAGBAGGAGCTGGGGCTGCGCTGACTCTACAGGTGCGAC 2152
Qy 2153 TACCCAGAAAGCTCTAGGGAACTGCACTGGTCACTATCTGT 2212	Db 2213 GATACTCTCTGATGTGTCACCATCGTGCACACTGGGGCTCTCCAGATGCTCCACTATCTGT 1872
Qy 1813 AACATACTCTGATGTGTCACCATCGTGCACACTGGGGCTCTCCAGATGCTCCACTATCTGT 2212	Db 2213 GATACTCTCTGATGTGTCACCATCGTGCACACTGGGGCTCTCCAGATGCTCCACTATCTGT 1872
Qy 1873 ACCTCCCTCTGATCTACTGGATCTGCGCTGGTATCTCAGGTGIGTGCCTGGACC 1932	Db 2273 GTTTCCTCTGTCCTACTTGTGACTGCGCTGCTGATGAGGTGCTGTGAC 2332
Qy 2273 GTTTCCTCTGTCCTACTTGTGACTGCGCTGCTGATGAGGTGCTGTGAC 2332	Db 1933 CAGACTGGCCAGGCCAGAACATACCCCTAGAGAACTCAAAGAACCTCCAGTT 1992
Qy 2333 CAGACCAAGGCCAGGCCAGAACATACCCCTAGAGAACTCAAAGAACCTCCAGTT 1992	Db 1993 CATGTTTATTCTATAGAACATGATTCTGCTGGTGAAGAATGAAATGGTACCT 2052
Qy 2391 CATGTTTATTCTATAGAACATGATTCTGCTGGTGAAGAATGAAATGGTACCT 2052	Db 2391 CATGTTTGTCTCATACAGTGGCATGATTCTGCTGGTGAAGAATGAAATGGTACCT 2450
Qy 2053 TACCTAGAAAAGAGATAACAGATATACAGATTTGTCTCATAGAGGAACTTGCCCTGCGAG 2112	Db 2451 AACCTAGAGAAAGATGAGATCCAGATTCCTGCTCATAGAGGAACTTGCCCTGCGAG 2510
Qy 2451 AACCTAGAGAAAGATGAGATCCAGATTCCTGCTCATAGAGGAACTTGCCCTGCGAG 2510	Db 2113 ACCATGGAAATATCATCACTGCATGGAGAGCTAACATGTCATTTGTTG 2172
Qy 2511 AGCATGGAGAACATCATCAATTCTATGGAGAGTTACAGTCATCTTGCTG 2570	Db 2571 TCCTCCACTCTCATCAGAGTGGTGTGATTAATGACTCATTCACAT 2232
Qy 2173 TCTCCAACTTGTCTCAGAGTGGTGTGCTCATCGACTCATTTGCCATCACAT 2232	Db 2631 CTCTCCATGAAGCTCTGATTAATCTCTCTGAAACCCATTCCACAGAC 2690
Qy 2233 CTTCTCTATGAGGATCTAACTTAATCTCTACTGAAACCCATTCCACAGAC 2292	Db 2293 ACCATCCAAACAGTACCAAGGCTCATGAGGAGGACTTATTGCAAG 2352
Qy 2751 TGGCCAGGAGAAAGAACGGCTTGGCTAACATTAGCCGTTTAAAT 2412	Db 2690 TGGCCAGGAGAAAGAACGGCTTGGCTAACATTAGCCGTTTAAAT 2750
Qy 2413 ATGAA 2417	Db 2751 TGGCCAGGAGAAAGAACGGCTTGGCTAACATTAGCCGTTTAAAT 2810
Qy 2811 GTTAA 2815	Db 2811 GTTAA 2815
RESULT 9	
DV779572 LOCUS DV779572	LOCUS DV779572
DEFINITION Hw fat_64 050830 B01 Bos taurus CF-24-HW fat cDNA library Bob	DEFINITION Hw fat_64 050830 B01 Bos taurus CF-24-HW fat cDNA library Bob
ACCESSION DV779572	ACCESSION DV779572
VERSION 2.1	VERSION 2.1
KEYWORDS EST.	KEYWORDS EST.
SOURCE Bos taurus (cattle)	SOURCE Bos taurus (cattle)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.	ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 1342)	REFERENCE 1 (bases 1 to 1342)
AUTHORS Yoon,D.H., Lee,S.H., Park,B.W., Cho,Y.M., Lee,J.H., Kim,H., Kim,H.Y., Park,J.H., and Oh,S.J.	AUTHORS Yoon,D.H., Lee,S.H., Park,B.W., Cho,Y.M., Lee,J.H., Kim,H., Kim,H.Y., Park,J.H., and Oh,S.J.
JOURNAL Gene Expression Profiling of the Bovine liver, adipose, and skeletal muscle	JOURNAL Gene Expression Profiling of the Bovine liver, adipose, and skeletal muscle
COMMENT Unpublished (2005)	COMMENT Unpublished (2005)
COMMENT Contact: Dr. Du-Hak Yoon	COMMENT Contact: Dr. Du-Hak Yoon
COMMENT National Livestock Research Institute, RDA	COMMENT National Livestock Research Institute, RDA
COMMENT 564 Omokchun-dong, Suwon, 441-350, Korea	COMMENT 564 Omokchun-dong, Suwon, 441-350, Korea
ORIGIN	
Query Match Best Local Similarity 22.0%; Score 604.8; DB 10; Length 1342; Matches 678; Conservative 0; Pred. No. 2.6e-138; Mismatches 122; Indels 0; Gaps 0;	Query Match Best Local Similarity 84.8%; Score 604.8; DB 10; Length 1342; Matches 678; Conservative 0; Pred. No. 2.6e-138; Mismatches 122; Indels 0; Gaps 0;
Matches 678; Conservative 0; Pred. No. 2.6e-138; Mismatches 122; Indels 0; Gaps 0;	Matches 678; Conservative 0; Pred. No. 2.6e-138; Mismatches 122; Indels 0; Gaps 0;
Db 1623 GAAGATGGGTATATAAGGAGGGAAATCATTCATGTCATCTGTGACTTAAGGA 1682	Db 1623 GAAGATGGGTATATAAGGAGGGAAATCATTCATGTCATCTGTGACTTAAGGA 1682
Db 27 GAAGATGGTCTCTCAAGCCGGAACTATCATTCAATGTCCTGTGACTTAAGGA 86	Db 27 GAAGATGGTCTCTCAAGCCGGAACTATCATTCAATGTCCTGTGACTTAAGGA 86
Qy 1743 TAATGTTGACTTACCCAGAAAGTATAGGAGGAACTTCAAGGACTTCAATGTCGTA 1802	Qy 1743 TAATGTTGACTTACCCAGAAAGTATAGGAGGAACTTCAAGGACTTCAATGTCGTA 1802
Db 147 TAATGTTGACTTACCCAGAAAGTACAGAGGAGGCTGGGGAGACTTCAGGATCTGA 206	Db 147 TAATGTTGACTTACCCAGAAAGTACAGAGGAGGCTGGGGAGACTTCAGGATCTGA 206
Db 1803 ATTATCCCTGACATACATCTGATGTTGTCCTCCATGGTGCACCATGTCGTTGA 1862	Db 1803 ATTATCCCTGACATACATCTGATGTTGTCCTCCATGGTGCACCATGTCGTTGA 1862
Db 207 CTCTCTGCAACACAGCTCTCTGATGTCACCATGTCGTTGA 266	Db 207 CTCTCTGCAACACAGCTCTCTGATGTCACCATGTCGTTGA 266
Qy 327 TCTCTGACCTGACCTCTCTGATGTCATCTGATGTCATGTCGTTGA 386	Qy 327 TCTCTGACCTGACCTCTCTGATGTCATCTGATGTCATGTCGTTGA 386
Db 1983 CTCTCTGACCTGACCTCTCTGATGTCATCTGATGTCATGTCGTTGA 2042	Db 1983 CTCTCTGACCTGACCTCTCTGATGTCATCTGATGTCATGTCGTTGA 2042
Db 387 TCTCTGACCTGACCTCTCTGATGTCATCTGATGTCATGTCGTTGA 446	Db 387 TCTCTGACCTGACCTCTCTGATGTCATCTGATGTCATGTCGTTGA 446
Qy 2043 ATGGTACCTTACTTAGAAAGAGATAACAGATGTCATGAGGAACTTGT 2102	Qy 2043 ATGGTACCTTACTTAGAAAGAGATAACAGATGTCATGAGGAACTTGT 2102
Db 447 ATGGTACCTTACTTAGAAAGAGATAACAGATGTCATGAGGAACTTGT 506	Db 447 ATGGTACCTTACTTAGAAAGAGATAACAGATGTCATGAGGAACTTGT 506
Db 2103 CCTGGCAGAGATGGAGAATATCATCACTGTCATGAGGAGTTGCTCATGAGGAACTTGT 2162	Db 2103 CCTGGCAGAGATGGAGAATATCATCACTGTCATGAGGAGTTGCTCATGAGGAACTTGT 2162
Db 507 TGCTGGCAGAGATGGAGAATATCATCACTGTCATGAGGAGTTGCTCATGAGGAACTTGT 566	Db 507 TGCTGGCAGAGATGGAGAATATCATCACTGTCATGAGGAGTTGCTCATGAGGAACTTGT 566
Db 2163 CTGGTGTGCTCCCAACTTGTCCAGAGTGGTGTGCTCATGAGGAGTTGCTCATGAGGAACTTGT 2222	Db 2163 CTGGTGTGCTCCCAACTTGTCCAGAGTGGTGTGCTCATGAGGAGTTGCTCATGAGGAACTTGT 2222
Db 567 CTGGTGTGCTCCCAACTTGTCCAGAGTGGTGTGCTCATGAGGAGTTGCTCATGAGGAACTTGT 626	Db 567 CTGGTGTGCTCCCAACTTGTCCAGAGTGGTGTGCTCATGAGGAACTTGT 626
Db 2223 CCTCACACATCTCTGATGTGAGGATCTACTTATCTCATCTACTGAACTTGT 2282	Db 2223 CCTCACACATCTCTGATGTGAGGATCTACTTATCTCATCTACTGAACTTGT 2282
Db 627 CACCACTCTCTCATGAGGATCTACTTATCTCATCTGTGCTGATCCAT 686	Db 627 CACCACTCTCTCATGAGGATCTACTTATCTCATCTGTGCTGATCCAT 686
Db 2283 TCCACAGACAGATTCCTCCACAGTGTGCTCATGAGGAGCTGAGGAGTC 2342	Db 2283 TCCACAGACAGATTCCTCCACAGTGTGCTCATGAGGAGTC 2342
Db 687 TCCACAGACAGATTCCTCCACAGTGTGCTCATGAGGAGTC 746	Db 687 TCCACAGACAGATTCCTCCACAGTGTGCTCATGAGGAGTC 746
Db 2343 TATTTGCACTGGCCCAAGGAGAAAGAACACAGCTGGGTCTTGGGTAATTAGGC 2402	Db 2343 TATTTGCACTGGCCCAAGGAGAAAGAACACAGCTGGGTCTTGGGTAATTAGGC 2402
Db 747 TATTTGCACTGGCCCAAGGAGAAAGAACACAGCTGGGTCTTGGGTAACCTAAAGC 806	Db 747 TATTTGCACTGGCCCAAGGAGAAAGAACACAGCTGGGTCTTGGGTAACCTAAAGC 806

QY	2403 CGGTTTATATGAAATTAA 2422	Db	807 ATCCATTAAATTAACTGA 826
RESULT 10			
DEFINITION	DA673961 NETRP2 Homo sapiens cDNA clone NETRP2004649 5', mRNA sequence.	LOCUS	DA673961 NETRP2 Homo sapiens cDNA clone NETRP2004649 5', mRNA
ACCESSION	DA673961	VERSION	DA673961.1 GI:80920622
KEYWORDS	EST.	TITLE	Homo sapiens (human)
ORGANISM	Homo sapiens (human)	REFERENCE	881 ATGACAACCTGTCAAGTTCACTTAATTTCAGACTCUCAGAGTTAACCTAC 360
SOURCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo	AUTHORS	821 TGAATTACCTCACCAACCATGAAAGCACTGGAAATGCCGGTAGAGCTTCAT 880
COMMENT	1 (bases 1 to 573)	VERSION	761 ATGACAACCTGTCAAGTTCACTTAATTTCAGACTCUCAGAGTTAACCTAC 820
JOURNAL	Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yonezawa, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanabe, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.	COMMENT	361 TGAATTACCTCACCAACCATGAAAGCACTGGAAATGCCGGTAGAGCTTCAT 420
PUBLISHED	Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes	COMMENT	881 TCTTTGGCCAAACCTGTGGATACTTCATTAACACATGAACTCACCAGAGTTAACCTAC 940
COMMENT	Genome Res. 16 (1), 55-65 (2006)	JOURNAL	421 TCCTTGCCCCAACCTGTGGATACTTCATTAACACATGAACTCACCAGAGTTAACCTAC 480
FLJ Project (HRI Team)	Contact: Takao Isogai	PUBLISHED	941 TCTGTGAGAAGAATTTTACTTAAACACATGAACTCACCAGAGTTAACCTAC 1000
Helix Research Institute	2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan	COMMENT	481 TTCTGGAACCAAGTTTCTGTGTTACAGACAG 1033
Tel: 81-438-52-3975	Fax: 81-438-52-3986	COMMENT	541 TACGAACCAAGTTTCTGTGTTACAGACAG 573
Email: flj-cdha@nifty.com			
RESULT 11			
DEFINITION	DB143901 THYMU3 Homo sapiens cDNA clone THYMU3018225 5', mRNA sequence.	LOCUS	DB143901 THYMU3 Homo sapiens cDNA clone THYMU3018225 5', mRNA
ACCESSION	DB143901	VERSION	DB143901.1 GI:83521199
KEYWORDS	EST.	AUTHORS	1 (bases 1 to 564)
ORGANISM	Homo sapiens (human)	REFERENCE	Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yonezawa, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
SOURCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo	TITLE	Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of putative Alternative Promoters of Human Genes
COMMENT	Genome Res. 16 (1), 55-65 (2006)	JOURNAL	26-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
PUBLISHED	Contact: Takao Isogai	PUBLISHED	Tel: 81-438-52-3975
COMMENT	FLJ Project (HRI Team)	COMMENT	Fax: 81-438-52-3986
Helix Research Institute	2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan	COMMENT	Email: flj-cdha@nifty.com
Tel: 81-438-52-3975	Fax: 81-438-52-3986	COMMENT	NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
Email: flj-cdha@nifty.com		COMMENT	Location/Qualifiers
ORIGIN			
Query Match	Best Local Similarity 99.8%; Pred. No. 4.1e-130; Indels 0; Gaps 0;	FEATURES	1. . 564
Matches 572; Conservative 0; Mismatches 1;		Source	/organism="Homo sapiens"
OY			/mol_type="mRNA"
461 ATTTCAGGCCCTGCCCATCTGTAGGGATTGCAACTTACACTGAACTTCCTGG	520		/db_xref="NC_000913"
Db	1 ATTTCAGGCCCTGCCCATCTGTAGGGATTGCAACTTACACTGAACTTCCTGG		/clone="THYMU3018225"
521 GATGAGTGCTATGAGCTGCAAATTAGATTAGTTGCTCCAATGCTCACTGCTCAA	580		/tissue_type="thymus"
QY	641 AAATTCTGAATGCAAAACCTTCACCTGTGTTTCACCAACTAGTTATCGTATCC		/clone_id="THYMU3"
Db	61 GATGAGTGCTATGAGCTGCAAATTAGATTGCTCCAATGCTCACTGCTCAA		/note="Vector: PME18SFL3"
581 GTTATATCTTCGTTGATTAGAAATTATATAAGAAATGAGCAGAAAGTCTAC	640		
Db	121 GTTATATCTTCGTTGATTAGAAATTATATAAGAAATGAGCAGAAAGTCTAC		
180			
QY			
641 AAATTCTGAATGCAAAACCTTCACCTGTGTTTCACCAACTAGTTATCGTATCC	700		
Db	181 AAATTCTGAATGCAAAACCTTCACCTGTGTTTCACCAACTAGTTATCGTATCC		
240			

ORIGIN

Query Match 20.4%; Score 562.4; DB 9; Length 564;
 Best Local Similarity 99.8%; Pred. No. 7e-128; 1; Indels 0; Gaps 0;
 Matches 563; Conservative 0; Mismatches 0;

QY 2006 CATATGAGACATGATTCCCTGGTGAAGAATGGTACCTACCTAGAAAGC 2065
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1 CATATGAGACATGATTCCCTGGTGAAGAATGGTACCTACCTAGAAAGC 60
 Fax: 81-438-52-3986

Db 2066 AGATATACAGATTGCTCATGAGAGAGAGTTGCCCTGGCAAGAGCAGTGGAAG 2125
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 61 AGATATACAGATTGCTCATGAGAGAGAGTTGCCCTGGCAAGAGCAGTGGAAG 120
 Email: fjj-cdna@nifty.com

Db 2126 ATATCATCAACTGCATGAGAGAGAGTTGCCCTGGCAAGAGCAGTGGAAG 2185
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 121 ATATCATCAACTGCATGAGAGAGAGTTGCCCTGGCAAGAGCAGTGGAAG 180
 Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

QY 2186 TCCAGAGTGAATGGTCATAGAACCTTATGGCCATCACACTCTTGCCAA 2245
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 181 TCCAGAGTGAATGGTCATAGAACCTTATGGCCAA 240
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Db 2246 GATCTATAACTTAATCTCTACTGGAACCCATCCACAGAACGTTCCACA 2305
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 241 GATCTATAACTTAATCTCTACTGGAACCCATCCACAGAACGTTCCACA 300
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 QY 2306 AGTACCAACAACCTGAAGGCTCTCATGAGCGGGAATTATGCAAGGAGA 2365
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 301 AGTACCAACAACCTGAAGGCTCTCATGAGCGGGAATTATGCAAGGAGA 360
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 Db 2366 AAAGCAAACGGGGCTTGGCTAACATAGAGCCGCTTAAATGAAATRAC 2425
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 361 AAAGCAAACGGGGCTTGGCTAACATAGAGCCGCTTAAATGAAATRAC 420
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 QY 2426 TAGTCACTGAACAACATGATGAAATCTTAAAATTTGAAATTCACTTAGAA 2485
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 421 TAGTCACTGAACAACATGATGAAATCTTAAAATTTGAAATTCACTTAGAA 480
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 Db 2486 CCATATTAGTTGGATGATGTGAATAGTCAGTGTAACTGTCGAGGTGCCT 2545
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 481 CCATATTAGTTGGATGATGTGAATAGTCAGTGTAACTGTCGAGGTGCCT 540
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 QY 2546 CCATTATCCTATGCCCTAGGAA 2569
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 Db 541 CCATTATCCTATGCCCTAGGAA 564
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ORIGIN

Query Match 20.1%; Score 553; DB 9; Length 609;
 Best Local Similarity 100.0%; pred. No. 1.5e-125; 0; Indels 0; Gaps 0;
 Matches 553; Conservative 0; Mismatches 0;

QY 2 GAATTTGACATCATTCAGATGCTCTGGAAAGAGACAAACCTTTAGGATAGGCCACTGCA 61
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 Db 367 GAATTTGACATCATTCAGATGCTCTGGAAAGAGACAAACCTTTAGGATAGGCCACTGCA 116
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 QY 62 ACATCATGACCAAGAACAAAGAACCTATGTTAAAGGTCCTATTGTTGCCCTATGCA 121
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 Db 117 ACATCATGACCAAGAACAAAGAACCTATGTTAAAGGTCCTATTGTTGCCCTATGCA 176
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 57 GAATTTGACATCATTCAGATGCTCTGGAAAGAGACAAACCTTTAGGATAGGCCACTGCA 116
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 QY 122 TCATAATAGTTGAAACAGAATCCGTCTCGGAGGAAATGAAATTGAGTACAGT 181
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 177 TCATAATAGTTGAAACAGAATCCGTCTCGGAGGAAATGAAATTGAGTACAGT 236
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 182 CAAAGAGGCTTATTGATGTCAAAGACCTACCGCTGAAGAACACCAGTCTAGATA 241
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 237 CAAAGAGGCTTATTGATGTCAAAGACCTACCGCTGAAGAACACCAGTCTAGATA 296
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 242 TGTCCTGAGAACTACATGCTGAGCTCTGCTCTGAGCTTATCAGTTGA 301
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 Db 297 TGTCCTGAGAACTACATGCTGAGCTCTGAGCTTATCAGTTGA 356
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 QY 302 CAGTTTGGACTTCCATACAGAACCTGGACTCTGTTAGTTGTTCACTGA 361
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 Db 357 CAGTTTGGACTTCCATACAGAACCTGGACTCTGTTCACTGA 416
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 QY 362 ACCAGGATTAAGAATTGATTGATTATCTCATATCGTGCAGAAAGATACTGCCTC 421
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 Db 417 ACCAGGATTAAGAATTGATTGATTATCTCATATCGTGCAGAAAGATACTGCCTC 476
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 QY 422 CTATGTTGAGCTTCCATACAGAACCTGGACTCTGTTCACTGA 481
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 Db 477 CTATGTTGAGCTTCCATACAGAACCTGGACTCTGTTCACTGA 536
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 QY 482 GAAAGGATTTGCAACTTACACAGATTCTGGATTAGTGTATGAGCTG 541
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 Db 537 GAAAGGATTTGCAACTTACACAGATTCTGGATTAGTGTATGAGCTG 596
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 Db 542 AAAATTAGATT 554
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 Db 597 AAAATTAGATT 609
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

ORIGIN

FlJ Project (HRI Team)

Helix

Research Institute

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NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES

Source

1. .609

/organism="Homo sapiens"

/mol type="mRNA"

/db_xref="taxon:9606"

/clone="JCMIC2"

/note="Vector: pMB18SFL3"

/clone lib="JCMIC2"

/note="Vector: pMB18SFL3"

	ACCESSION	BG663497	QY	2015 AACATGATCTCGCCGGTGAAGTGTAATTGGTACCTTACTAGAAAGAGATATAC
	VERSION	BG663497.1	GI:14351134	
	KEYWORDS	EST'		
	SOURCE	Mus musculus (house mouse)		
	ORGANISM	Mus musculus		
REFERENCE	Eukaryota: Metazoa; Chordata: Craniata: Vertebrata; Buteleostomi; Mammalia; Eutheria; Eumetazoans; Glires; Rodentia; Scurognotathi; Muridae; Murinae; Mus.		QY	2075 AGATTTCCTCATGAGAGACTTGTCCCTGGCAAGAGATTGGGAATAATCTCA
AUTHORS	1 (bases 1 to 772)		Db	481 GGATGATTCCTGCCTGGTGAAGAACATTACCCAACTTAGAGAAGATGACCC
TITLE	NIM-MGC http://mgc.nci.nih.gov/		QY	541 AGATTTCCTCATGAGAGACTTGTCCCTGGCAAGAGATTGGGAATAATCTCA
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		Db	600
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov		QY	2135 ACTGATCTGAGAGACTTGTCCCTGGCAAGAGATTGGGAATAATCTCA
Tissue Procurement	Jeffrey E. Green, M.D.		Db	661 ACTGGTGTCTATGAGACTCTATTGGCCATCAAGATCTCTTCATGAGCTGT
CDNA Library Preparation	Life Technologies, Inc.		QY	2195 ACTGGTGTCTATGAGACTCTATTGGCCATCAAGATCTCTTCATGAGCTGT
CDNA Library Arrayed By	The I.M.A.G.E. Consortium (ILNL)		Db	720
DNA Sequencing By	Incyte Genomics, Inc.		QY	2254 AACTTATCCATCTTACTGAAACCATTCCACAGACACATTCCACAA
Clone distribution	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:		Db	730
Plate	LLM11994	row: o column: 15		721 AACTTAATCTCATCTGCTGGCA-CCATACCCAGTACTCGATGCCAACAA
High quality sequence stop: 735.				772
FEATURES	Location/Qualifiers			
source	1. 772 /organism="Mus musculus" /mol_type="mRNA" /strain="NBB/N" /db_xref="taxon:10090" /clone="IMAGE:4986086" /lab_host="DH10B (T1 phage-resistant)" /clone_libr="NCI CGAP_Cox4" /note="Organ: colon; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.6 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."			
ORIGIN				
Query Match	19.2%; Score 529.8; DB 2; Length 772;		RESULT	14
Best Local Similarity	82.0%; Pred: No. 9e-120;		LOCUS	CK980631
Matches	634; Conservative 0; Mismatches 137; Indels 2; Gaps 2;		DEFINITION	CK980631
Qy	1535 GATGTTGGCAGGTTAGACGCTTCGATGATCATGATGACAACTCAGTTCCACC		ACCESSION	4112385 BARC 9BOV Bos taurus mRNA clone 9BOV41_D08 5', mRNA
Db	1 GGTGGGGGGCTTCAGACGCTTCGTCGGTCACTGACATACTCAGTTCCATC		VERSION	CK980631.1 GI:45498611
Qy	1595 CATCGCTGATTCCTCCAGAGCTGCCAGAAAGATGAGGTCTATAAAGCAGGGCAATC		KEYWORDS	EST.
Db	61 OCTCTGAGGAGTTCTCCAGAGCTGTCAGAAATTAGTCCTAACAGGGAAACACC		SOURCE	Bos taurus (cattle)
Qy	1655 CATTCCAATGAGCATGTGAGCTGGAGGACTTGTGAGAGATTCAGTCTAAC		ORGANISM	Bos taurus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
Db	121 CATTCCAATGAGCATGTGAGCTGGAGGACTTGTGAGAGATTCAGTCTAAC		REFERENCE	1 (bases 1 to 698)
Qy	1715 AGATGTTAGAGGGCTGCTGATTCTATAGTGACTACCCAGAAGTTAGAGAA		AUTHORS	Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harnay, G.P., Boak, S., Rubenfield, M. and Gasbarre, L.C.
Db	181 AGTGGGGAGGGCTGCTACTCTACAGTGTCAGTCTAGGGAA		TITLE	Production of EST from cDNA libraries derived from immunologically activated bovine gut
Qy	1775 GCCCACTAAGGACTTCACTGTCTGAATTATCTGCAACATAACTCTGGTATGTCA		JOURNAL	Unpublished (2004)
Db	241 CTGCACTGAGGACTTCACTGTCTGAATTATCTGCAACATAACTCTGGTATGTCA		COMMENT	Contact: Ted S. Sonstegard
Qy	1835 OCATCGGTGCCACCATGCTGGTGTGGCTGACTCTGACTCCCTCTGCTACTCTGG			Bovine Functional Genomics Laboratory
Db	301 OCATCGGGCCACTATCTGGTGTGGCTGACTCTGGCTTCTCTGCTACTCTGG			Animal and Natural Resources Institute
Qy	1895 ATCTGGCTTATCTCGAGGTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG			Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Db	361 ACCTGGCTCTGGTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG			Tel: 301-5048116
Qy	1955 ACATACCTTGAAGACTCCAAAGAACCTCCAGTTCTGCTTATTTCATAGTG			Fax: 301-5048114
Db	421 ACATCCCTTGAAGACTCCAAAGAACCTCCAGTTCTGCTTATTTCATAGTG			Email: tads@nri.barc.usda.gov
Qy	1895 ATCTGGCTTATCTCGAGGTTGGCTGGCTGGCTGGCTGGCTGGCTGG			Single pass sequencing. Bases called and trimmed with phred 0.00925 using options -trim alt "-" -trim fasta. Vector identified by cross match using options -minmatch 12 -minscore 12
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Qy	1955 ACATACCTTGAAGACTCCAAAGAACCTCCAGTTCTGCTTATTTCATAGTG			Seq primer: CCCAGTACGGCTGGCTAAACG
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Db	361 ACCTGGCTCTGGTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG			
Qy	1955 ACATACCTTGAAGACTCCAAAGAACCTCCAGTTCTGCTTATTTCATAGTG			
Db	421 ACATCCCTTGAAGACTCCAAAGAACCTCCAGTTCTGCTTATTTCATAGTG			

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QY	1968	AGAACTCCAAGAAACCTCCAGTTCTAGCTTATTCATATAGAAGCTTGATCTGC	2027		
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QY	2089	TGAGGGAACCTTGTCCTGCCAGAACGCTTGGAATAATCATACTGCATGAGAA	2147		
Db	547	TGAGGGAACCTTGTCCTGCCAGAACGCTTGGAATAATCATACTGCATGAGAA	606		
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KEYWORDS	EST.				
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ORGANISM	Macaca mulatta				
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REFERENCE	1 (bases 1 to 684)				
AUTHORS	Katz, M.G., Bungarner, R., Korth, M., Feldman, R., Amjadi, M. and Holzman, T.				
TITLE	Expressed sequence tags from Rhesus macaque spleen				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Holzman, T				
Katze Lab					
University of Washington					

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Box 358070, Seattle, WA 98195-8070, USA
 Tel: 206 732 6155
 Fax: 206 732 6055
 Email: ted@locke.hsl.washington.edu
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FEATURES source

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

0; Mismatches

Indels

31; Gaps

5;

Db

1 AAAAGATATGGTACTCTAGTCAGAGAAGGTAGATTTGCTTCATGAGAGA

60

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1 ACTTGTCTCTGGTAAAGAGATATATCATCACTGAGTCACTGCTTGTGAGAAGT

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